

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.0526 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKSLRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80.*
1: Pir1.*
2: Pir2.*
3: Pir3.*
4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	2086	100.0	400	1 JCI1428	ketol-acid reducto
2	1508.5	72.3	395	1 A24709	ketol-acid reducto
3	1494.5	71.6	404	2 T40532	ketol-acid reducto
4	497	23.8	333	2 F70407	acetohydroxy acid
5	486	23.3	332	2 H75044	ketol-acid reducto
6	484.5	23.2	331	2 AC1694	ketol-acid reducto
7	483	23.0	331	2 C69644	ketol-acid reducto
8	480.5	23.0	331	2 AB1323	ketol-acid reducto
9	469.5	22.5	581	2 T06825	ketol-acid reducto
10	465	22.3	591	1 S30145	ketol-acid reducto
11	465	22.3	591	2 T45681	ketol-acid reducto
12	463	22.2	335	2 C90204	ketol-acid reducto
13	463	22.2	337	2 A96911	ketol-acid reducto
14	459.5	22.0	340	2 C84032	ketol-acid reducto
15	458.5	22.0	336	2 D72362	ketol-acid reducto
16	456	21.9	331	2 AD2095	ketol-acid reducto
17	450	21.6	348	1 F64492	ketol-acid reducto
18	444	21.3	367	1 A47037	ketol-acid reducto
19	442.5	21.2	334	2 F89997	alpha-keto-beta-hy
20	438.5	21.0	595	1 S17180	ketol-acid reducto
21	432.5	20.7	336	2 G95051	ketol-acid reducto
22	432.5	20.7	340	2 C97922	ketol-acid reducto
23	429	20.6	363	2 C75387	ketol-acid reducto
24	427.5	20.5	337	2 C81801	ketol-acid reducto
25	427.5	20.5	337	2 F81066	ketol-acid reducto
26	415	19.9	340	2 B86778	ketol-acid reducto
27	414.5	19.9	332	2 H69497	ketol-acid reducto
28	409	19.6	344	1 S35140	probable ketol-aci
29	405.5	19.4	333	2 A69059	ketol-acid reducto

30	19.4	340	2	G81411	ketol-acid reducto
31	393	18.8	338	2 E83059	ketol-acid reducto
32	387	18.6	338	1 C48648	ketol-acid reducto
33	381	18.3	366	2 E82634	ketol-acid reducto
34	378	18.1	332	2 T35830	acetolactate synth
35	360	17.3	333	1 JC5166	ketol-acid reducto
36	349	16.7	333	2 H87120	ketol-acid reducto
37	349	16.7	343	2 T45415	ketol-acid reducto
38	340	16.3	333	2 D70855	probable ilvC prot
39	335	16.1	339	2 G87511	ketol-acid reducto
40	329.5	15.8	339	2 AB3330	ketol-acid reducto
41	329	15.8	330	1 B64561	ketol-acid reducto
42	329	15.8	339	2 AE2824	ketol-acid reducto
43	329	15.8	339	2 D97602	hypothetical prote
44	325	15.6	330	2 A71945	ketol-acid reducto
45	321	15.4	491	1 ISECKR	ketol-acid reducto

ALIGNMENTS

RESULT 1

JCI1428

ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa

N;Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase

C;Species: Neurospora crassa

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C;Accession: JCI1428

R;Sista: H. J. Bowman, B.

(Gene 120, 115-118, 1992)

A;Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-be

A;Reference number: JCI1428; MUID:93013010; PMID:1398116

A;Accession: JCI1428

A;Molecule type: DNA

A;Residues: 1-400 <SIS>

A;Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:G168821; PIDN:1

C;Genetics:

A;Gene: ilv-2

A;Map position: V

A;Introns: 68/1; 78/3; 170/3; 392/3

C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom

C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase

F;87-273/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 100.0%; Score 2086; DB 1; Length 400;
Best Local Similarity 100.0%; Pred. No. 6.9e-146;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQVRGVKTMDFA 60

Db 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQVRGVKTMDFA 60

QY 61 GHKEEVEHRAADWPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGNLNIVGVKNGKSW 120

Db 61 GHKEEVEHRAADWPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGNLNIVGVKNGKSW 120

QY 121 EDALQDQWPGKXNLFVDDEAISRGTIVMNLSDAAQSETWPHIKPOITKGTLYFSGHGS 180

Db 121 EDALQDQWPGKXNLFVDDEAISRGTIVMNLSDAAQSETWPHIKPOITKGTLYFSGHGS 180

QY 181 PVFKDLTKVEVPTDNDVILVAPKSGRTVRSILFREGGINSSFAVQDVTGKAKEKAVAL 240

Db 181 PVFKDLTKVEVPTDNDVILVAPKSGRTVRSILFREGGINSSFAVQDVTGKAKEKAVAL 240

QY 241 GVAVSGGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSAFNETVE 300

Db 241 GVAVSGGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSAFNETVE 300

QY 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIQWTPFKDALKPVFNLYDSVKNGBDERKR 360

Db 301 EATQSLYPLIGAHGMDWMDACSTTARRGAIQWTPFKDALKPVFNLYDSVKNGBDERKR 360

QY 361 SLEYNQPDYRERYEAELEIRNLEIWRAGKSLRPENQK 400

Db 361 SLEYNQPDYRERYEALDEIRNLEIWRAGKRSILRPENQK 400

RESULT 2

A24709

ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)

N;Alternate names: acetoxyhydroxyacid reductoisomerase ILV5; protein YLR3

C;Species: Saccharomyces cerevisiae

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C;Accession: A24709; S51463

R;Petersen, J.G.L.; Holmberg, S.

Nucleic Acids Res. 14, 9631-9651, 1986

A;Title: The ILV5 gene of Saccharomyces cerevisiae is highly expressed.

A;Reference number: A24709; MUID:87117524; PMID:3027658

A;Accession: A24709

A;Molecule type: DNA

A;Residues: 1-395 <FET>

A;Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:g3826; PIDN:R;Du, Z.

submitted to the EMBL Data Library, December 1994

A;Description: The sequence of S. cerevisiae cosmid 9638.

A;Reference number: S51459

A;Accession: S51463

A;Molecule type: DNA

A;Cross-references: 1-395 <DUZ>

A;Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:g609396; PIDN:ARAB67753.1; PI

C;Genetics:

A;Gene: SGD:ILV5; MIPS:YLR355C

A;Cross-references: SGD:S0004347; MIPS:YLR355C

A;Map position: 12R

C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom

C;Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase

F;81-267/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 72.3%; Score 1508.5; DB 1; Length 395;

Best Local Similarity 73.6%; Pred. No. 2.1e-103;

Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;

QY 7 TKALRPLARQLATPAVQRTFTFAAASAVASVAVKAAVAPARQV-----RGVKTMDFA 60

Db 4 TQARLICSRVITA---KRTF---ALATRAA-----AYSRAARFVKPMITTRLKQINFG 54

QY 61 GHKEEYERADWPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGLNVIQVRKNGKSW 120

Db 55 GTVETVYERADWPREKLLDYFKNDTLALIGYSGQHGQGLNLDNGLNVIQVRKDGASW 114

QY 121 EDIAIQGVVPGKMLFDVDEIRSGTIVMNLSDAAQSETWPHIKPQITKGLTYFSHGFS 180

Db 115 KAAIEDGVVPGKMLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKGLTYFSHGFS 174

QY 181 PVFKDLTKVEVPTDQVILVAPKSGRTVRSIFREGRGINSFAYVQDVTGKAKEKAVAL 240

Db 175 PVFKDLTKVEVPTDQVILVAPKSGRTVRSIFREGRGINSFAYVQDVTGKAKEKAAQAL 234

QY 241 GVAVGSGLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 300

Db 235 AVAIGSGYVYQTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 294

QY 301 EATQSLYPLIGHGMWDMFDACSTTARRGAIDWTPKFDKALPVPFNLLYDSVKNGDERK 360

Db 295 EATQSLYPLIGHGMWDMFDACSTTARRGAIDWTPKFDKALPVPFNLLYDSVKNGDERK 354

QY 361 SLEYNQPDYRERYEALDEIRNLEIWRAGK--RSILRPENQ 399

Db 355 SLEFNQPDYREREKLELDTIRNMEIWKVKEVRKLRPENQ 395

RESULT 3

T40532

ketol-acid reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomy

C;Species: Schizosaccharomyces pombe

C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004

C;Accession: T40532; T43303; T42540

R;Purnelle, B.; Goffeau, A.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.

submitted to the EMBL Data Library, May 1998

A;Reference number: Z21935

A;Accession: T40532

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: DNA

A;Residues: 1-404 <PUR>

A;Cross-references: UNIPROT:P78827; UNIPARC:UPI000012D527; EMBL:AL023288; NID:g5832408; I

A;Experimental source: strain 972h-; cosmid c56F2

R;Kawamukai, M.

submitted to the EMBL Data Library, December 1997

A;Description: S.pombe ILV5 homolog.

A;Reference number: Z22407

A;Accession: T43303

A;Status: translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 262-404 <KAW>

A;Cross-references: UNIPARC:UPI000168765; EMBL:AB009603; NID:g2696653; PIDN:BAA24000.1;

R;Yoshioka, S.; Kato, K.; Nakai, H.; Okayama, H.; Nojima, H.

DNA Res. 4, 363-369, 1997

A;Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.

A;Reference number: Z17323; MUID:98162722; PMID:9501991

A;Accession: T42540

A;Status: preliminary; translated from GB/EMBL/DBDJ

A;Molecule type: mRNA

A;Residues: 1-37, 'R', 39-40, 'W', 42-91, 'S', 93-237, 'T', 239-274, 'P', 276-296, 'P', 298-393, 'G', '3

A;Cross-references: UNIPARC:UPI0001690FE; EMBL:D89175; NID:g1749557; PIDN:BAAL3837.1; PI

C;Genetics:

A;Gene: SPDB:SPBC56F2.12

A;Map position: 2

C;Function:

A;Pathway: branched-chain amino acid biosynthesis

C;Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom

C;Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase

F;88-274/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 71.6%; Score 1494.5; DB 2; Length 404;

Best Local Similarity 69.7%; Pred. No. 2.4e-102;

Matches 287; Conservative 52; Mismatches 46; Indels 27; Gaps 4;

QY 2 AARNCTKALRPL-ARQLATPAVQRTFTFAAASAVASVAVKAAVAPARQ-----Q 50

Db 6 SSEWAKALRTWGSRLATRS-----SWARTIAAPSRFAPRMTAPLMQ 51

QY 51 VRGVTMDPAGHKEVHERADWPAEKLLDYFKNDTLALIGYSGQHGQGLNLDNGLNVI 110

Db 52 TRGMRVMDPAGTKENWERSDWPREKLVDFKNDTLALIGYSGQHGQGLNLDNGLNVI 111

QY 111 VQVRKNGKSWEDAIQDGVVPGKMLFDVDEIRSGTIVMNLSDAAQSETWPHIKPQITKG 170

Db 112 VQVRKDGASWQAIEDGVVPGKTLFPVEATIKGSIIMNLLSDAAQSETWPHIKPQITKG 171

QY 171 KTLYFSHGFSVPFKDLTKVEVPTDQVILVAPKSGRTVRSIFREGRGINSFAYVQDVT 230

Db 172 KTLYFSHGFSVIFKQDTKIHPPKQDVVILVAPKSGRTVRLTFKEGRGINSFAYVQDVT 231

QY 231 GKAKEKAVAGVAVGSGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGH 290

Db 232 GKAKEKAVAGVAVGSGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGH 291

QY 291 PSEAFNETVEATQSLYPLIGHGMWDMFDACSTTARRGAIDWTPKFDKALPVPFNLLYD 350

Db 292 PSEAFNETVEATQSLYPLIGHGMWDMFDACSTTARRGAIDWTPKFDKALPVPFNLLYD 351

QY 351 SVKNGDERKRSLEYNQPDYRERYEALDEIRNLEIWRAGK--RSILRPENQ 400

Db 352 NVENGNEAKRSLEYNQPDYRERYEALDEIRNLEIWRAGK--RSILRPENQ 403

RESULT 4

F70407

acetohydroxy acid isomeroreductase - Aquifex aeolicus

C:Species: Aquifex aeolicus
C>Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C:Accession: F70407
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O'V.
Nature 392, 353-358, 1998
A>Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70407
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-333 <AOP>
A:Cross-references: UNIPROT:Q67289; UNIPARC:UPI0000056582; GB:AE000730; NID:G2983674; PI
A:Experimental source: strain VF5
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
F;21-203/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.8%; Score 497; DB 2; Length 333;
Best Local Similarity 34.7%; Pred. No. 4.6e-29;
Matches 115; Conservative 70; Mismatches 124; Indels 22; Gaps 9;

78 LDYFKNDTLALIGYSGHQGLNLRDNLNIVGVKNGKSWEDAIQDGVVPGKNLFDV 137

Db 12 LDILKDVIALIGYSGHQGHALNLRDNLNIVGVKNGKSWEDAIQDGVVPGKNLFDV 67

Qy 138 DEAISRGITVMNLLSDAAQSETWPH-IPKQITKTKTLYFSGHGFSPVFKDLTKVEVPD 196

Db 68 REAAKRAIIMFLIPDTVQPEYKNEVEPELNSKTLFAHGFNIHQIIVP---PKD 124

Qy 197 VILVAPKSGRTVRSFLPREGGINSSPAVQDVTGKAKKAVAGVGS--GYLYETTF 254

Db 125 VFMVAPKSGHLVRWMTYEGKGVPAVVAIHQDASGTCCKALAYAKGIGATRA 184

Qy 255 EKEVYSDLYGRCGLMGHGMFLAQYEVLRERGHSPSAFNETVEATOSLYPLI 314

Db 185 KEETETDLFGQVLCQGLGATLIIKAGFETLVNAGYQPEVAFECLEH-LKLI 243

Qy 315 MDWMFDACSTTARRGALDWTPTKFKDALKPNNLYDSVKNDEKRSLEYN--SQ 370

Db 244 ISGWRYSISDTAKYDVTGRERIYKVKVPVWEKLEBIQGEFAREWILENKA 303

Qy 371 ---RER---YEAELEIRNLEIWRAGKRSR 395

Db 304 LLERDRHLVEKVGEEELKMPW-LGKKELK 333

RESULT 5

H75044
ketol-acid reductoisomerase (ilvC) PAB0889 - Pyrococcus abyssi (strain Orsay)
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004
C:Accession: H75044
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A:Reference number: A75001
A:Accession: H75044
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-332 <KAW>
A:Cross-references: UNIPROT:Q9U209; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: ilvC; PAB0889
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
F;24-206/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.3%; Score 486; DB 2; Length 332;
Best Local Similarity 37.8%; Pred. No. 3e-28;
Matches 122; Conservative 63; Mismatches 120; Indels 18; Gaps 9;

Qy 75 EKLLDVPKNDTLALIGYSGHQGLNLRDNLNIVGVKNGKSWEDAIQDGVVPGKNL 134

Db 12 EVSMDILKDKTAVIGYGNQGEAQAKMRDSDGVHVLGRPSGSSWRAEKDGF---EV 67

Qy 135 FVDVDEAISRGITVMNLLSDAAQSETW-PHIKPOITKTKTLYFSGHGFSPVFKDLTKVEPT 193

Db 68 YTIEEAVKRAIDIVHILIPDLVQPKVREHIEPIELRGQALGFGHGFNIHQIIVP---PE 124

Qy 194 DVDVILVAPKSGRTVRSFLPREGGINSSPAVQDVTGKAKKAVAGVGS--SGYLY 250

Db 125 YVDVIVVAPKSGKRVREKVLGFGVPALVAVQDVTGNKADLALAKAIGCTRAGVI- 183

Qy 251 ETTPEKEVYSDLYGRCGLMGHGMFLAQYEVLRERGHSPSAFNETVEATOSLYPLI 310

Db 184 ETTFKDETETDLFGQVLCQGLGATLIIKKGFEVLVGLGPPPELAYFEACNEA-KLIMDLI 242

Qy 311 GAHGMDFDACSSTARRGALDWTPTK-FKDALKPNNLYDSVKNDEKRSLEYNSQPD 369

Db 243 YERGFTGMLKAVSDTAKYGLGTVPKVIDDHVKENMKKFAERVRSGEFAK---EWISKAD 299

Qy 370 -YRERYEAELEIRNLEIWRAGK 391

Db 300 KASEVLEELMKPIEHEIEKVGR 322

RESULT 6

AC1694

ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
C:Species: Listeria innocua
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AC1694
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dusauret, O.; Entian, K.D.; Feihl, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A.; Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1694
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <GLA>
A:Cross-references: UNIPARC:UPI00000CC759; GB:AL592022; PIDN:CAC97323.1; PID:g16414607;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom

Query Match 23.2%; Score 484.5; DB 2; Length 331;
Best Local Similarity 38.2%; Pred. No. 3.8e-28;
Matches 125; Conservative 50; Mismatches 117; Indels 35; Gaps 10;

Qy 79 DYFKND-----TLALIGYSGHQGLNLRDNLNIVGVKNGKSWEDAIQDGVVPGKN 133

Db 8 DAVKNALREGKTVAVIGYSGHQGHASQNLNRDNNVIGIRE-GKSAESARNDGF---D 62

Qy 134 LPDVEDAISRGITVMNLLSDAAQSETWPH-IPKQITKTKTLYFSGHGFSPVFKDLTKVEVP 192

Db 63 VYVSSEAEAKADVIMILLPDETQGETYEINEIKNALVPAHGFNIHF---DVINPP 119

Qy 193 TDVDVILVAPKSGRTVRSFLPREGGINSSPAVQDVTGKAKKAV--ALGVAVSGSYLY 250

Db 120 SDVDVFLVAPKSGHLVRRTFVEGGAVPSLFIAYIQDATGNARDTALSAYAKIGATRA 179

Qy 251 ETTPEKEVYSDLYGRCGLMGHGMFLAQYEVLRERGHSPSAFNETVEATOSLYPLI 310

Db 180 ETTFKDETETDLFGQVLCQGLGATLIIQAGFETLVAGYQPELAYFEVLHE-MKLI 238

Qy 311 GAHGMDFDACSSTARRGALDWTPTKFKDALKPNNLYDSVKNDEKRSLEYNSQPD 354

Db 239 YEGGMEKMRHSISNTAEYG--DYVSGPRVVTADTKKAMKEVLTDIQNGNFAKSFIDDNKN 296

QY 355 GDERKRSLEYNQPDYRERYEAELDEI 381
Db 297 GFKEFHMRKEQQGHQIEKVGAEUREM 323

RESULT 7
C69644
ketol-acid reductoisomerase ilvC - Bacillus subtilis
C/Species: Bacillus subtilis
C/Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C/Accession: C69644
R/Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berton
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997

A/Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallen
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.P.
Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
A/Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mausel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaite, Y.; Sato, T.; Scanlon,
A/Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tognoni, V.; Uchiyama,
T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K
A/Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A/Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A/Reference number: A69580; PMID:98044033; PMID:9384377

A/Accession: C69644
A/Status: preliminary; nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-342 <KUN>
A/Cross-references: UNIPROT:P37253; UNIPARC:UPI0000038DER; GB:Z99118; GB:AL009126; NID:9
A/Experimental source: strain 168
C/Genetics:
A/Gene: ilvC
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
F;21-202/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 23.2%; Score 483; DB 2; Length 342;
Best Local Similarity 38.3%; Pred. No. 5.2e-28;
Matches 119; Conservative 58; Mismatches 108; Indels 26; Gaps 10;

QY 80 YPKND-----TLALIGYSGHGQGLNRDNGNLNIVGVKNGKSWEDAIQDGWVP 130
Db 5 YNGDITKENVLAKTVAVIGYSGQGHANLNKESGVDVIVGRQ-GKSFYQAQED-----59

QY 131 GKPLFDVDEAISRTIVMNLSDAAQSETW-PHIKQITKGKTLVPSHGFSVPFKDLTKV 189
Db 60 GHKVFVKAAQAIEIIVLLPDEQQKVEYAEIKDELTAGKSLVFAHGFNVHFHIVP- 118

QY 190 EVPTDVIDVLVAPKSGRTVRSLFREGRGINSFVYQDVTKAKEKAVLGAVG--S 246
Db 119 --PADVDVFLVAPKPGCHLVRRTYEQAGVPALFAIYQDVTEARDKALAYAKGIGARA 176

QY 247 GYLTYETFEKVEYSDLYGERGCLMGHGMFLAQYVLRERHSPSEAFNETVEEATQSL 306
Db 177 GVL-ETTFKEETETDLFGQAVLCGGSLVAVRAGFTLLEAGYQPELAYFECLHE-LKLI 234

QY 307 YPLIAGHGMDFDACSTTARRGAIDWTTPKFDA-LKVPFNILYDSVKNGDERKRSLEYN 365
Db 235 VDLMYEEGLAGMRYISIDTAQWGDVFSVGRVVDKVKESMKVLDIQNGTAKEWIVEN 294

QY 366 SQPDYRERYEA 376
Db 295 QV--NRPRFNA 303

RESULT 8
AB1323
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC (imported)
C/Species: Listeria monocytogenes
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004

C/Accession: AB1323
R/Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.;
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A/Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Maqueno, E.; Maitournam, A.; Mat
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A/Title: Comparative genomics of Listeria species.
A/Reference number: AB1077; PMID:21537279; PMID:11679669
C/Accession: AB1323
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-331 <GLA>
A/Cross-references: UNIPARC:UPI0000054PF8; GB:NC_003210; PIDN:CAD00064.1; PID:gl6411439;
A/Experimental source: strain EGD-e
C/Genetics:
A/Gene: ilvC
C/Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom
Query Match 23.0%; Score 480.5; DB 2; Length 331;
Best Local Similarity 37.9%; Pred. No. 7.5e-28;
Matches 124; Conservative 52; Mismatches 116; Indels 35; Gaps 10;

QY 79 DYFKND-----TLALIGYSGHGQGLNRDNGNLNIVGVKNGKSWEDAIQDGWVP 133
Db 8 DAVKNNALGKTVAVIGYSGQGHANLNKESGVDVIVGRQ-GKSFYQAQED-----D 62

QY 134 LFDVDEAISRTIVMNLSDAAQSETWPH-IKQITKGKTLVPSHGFSVPFKDLTKVEVP 192
Db 63 VYSVSEADKADVIMILLPDETQGETYENEIKPNLKAGNSLVFAHGFNIHF--DVINFP 119

QY 193 TDVDVLVAPKSGRTVRSLFREGRGINSFVYQDVTKAKEKAV--ALGVAVSGGYLY 250
Db 120 SDVDVFLVAPKPGCHLVRRTYEQAGVPSLFAIYQDVTGNARDTALSVAKGIGATRAVY 179

QY 251 ETTFEKVEYSDLYGERGCLMGHGMFLAQYVLRERHSPSEAFNETVEEATQSLYPLI 310
Db 180 ETTFEETETDLFGQAVLCGGATHLIOAGFTLVAGYQPELAYFEVLHE-MKLIVDLM 238

QY 311 GAHGMDFDACSTTARRGAIDW-----TPFKDALKVPNNL-----YDSVK 354
Db 239 YEGGKMKRHSISNTAEYV--DYVSGPRVVTADTKKAMKEVLTDIQNGNFAKSFINDNKN 296

QY 355 GDERKRSLEYNQPDYRERYEAELDEI 381
Db 297 GFKEFHMRKEQQGHQIEKVGAEUREM 323

RESULT 9
T06825
ketol-acid reductoisomerase (EC 1.1.1.86) - garden pea
C/Species: Pisum sativum (garden pea)
C/Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 05-Oct-2004
C/Accession: T06825
R.Zhu, X.
submitted to the EMBL Data Library, August 1998
A/Reference number: Z15837
A/Accession: T06825
A/Status: preliminary; translated from GB/EMBL/DBDJ
A/Molecule type: mRNA
A/Residues: 1-591 <ZHU>
A/Cross-references: UNIPROT:O82043; UNIPARC:UPI000012DS26; EMBL:Y17796; PIDN:CAA76854.1
A/Experimental source: cv. G2
C/Genetics:
A/Gene: pgaair
C/Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol
C/Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F.113-311/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.5%; Score 469.5; DB 2; Length 581;
Best Local Similarity 26.8%; Pred. No. 1.1e-26;
Matches 140; Conservative 62; Mismatches 128; Indels 193; Gaps 10;

QY 1 MAA--RNCTKALRPLARLATP-----AVORTFVAASAVRASVAV 40
 DB 1 MAATVSSCTAISASSKTLAKPAASAPNTLSPSKLSPQIRARRSITVGSALGAT--- 57
 QY 41 KAAAPARQOVRGVKTMDF-----AGHKEEYHERADWPAEKLLDYFNK-DTLA 87
 DB 58 KVSAPPATHPV-----SLDFETSVFKKERNVLGAGHEEYVIRGRDLPHLLPDAFKGIQIG 113
 QY 88 LIGVSGQHGGGLNLRD-----NGLNIVGVKNGKSWEDAIQGWVPGK-NLFDVDEA 140
 DB 114 VIGWGSQGPAAQNLRDLSVEAKSDIVVKGVLKRGSSSFNEAREAGFSEKGTGLDIWET 173
 QY 141 ISRGITVNNLLSDAAQSTWPHIKPQITKGTLYFSGHGSFVFKDLTKVVEPTDVLV 200
 DB 174 ISGDLVLLLSDSAQADNYEKI FSHLKPNSILGLSHQSLGLDPFKNFSVIAV 233
 QY 201 APKSGRTVRSFLRGR-----GINSSPANYQDVTKAKAKAVALGVAVGSGYLTYTFE 255
 DB 234 CPKMGPSVRLYVQKKEINGAGINSFVGHQVDVGRATNVALGWSVALGSPFTFATLE 293
 QY 256 KEVTSDDLGERGCLMGGIHG----- 275
 DB 294 QEYKSDIFGERGILLGAVHGIVESLFRYRTENGMSDLAYKNTVESITGVISTQGM 353
 QY 276 ----- 275
 DB 354 LAVINALSEDKGFEKAYSASFPCMEILYECYEDVASGSEIRSVVLGRFRFYKEKGLP 413
 QY 276 -----MFLAQEVLRLRERHSPSEA 294
 DB 414 AFPWGIKIDQTRMKVGRVSTRPAGDLGLPYPTAGVVFVAMMAQIEVLKKGHSYSEI 473
 QY 295 FNETVEBATOGLYPLIGHGMDWMDACSTTARRGAIDWTPKF 337
 DB 474 INESVIESVDSLNPFMHARGVSFVMDNCSTTARLGSRKWAPRF 516
 RESULT 10
 S30145
 ketol-acid reductoisomerase (EC 1.1.1.86) precursor - Arabidopsis thaliana
 N/Alternate names: acetohydroxy acid isomeroeductase
 C/Species: Arabidopsis thaliana (mouse-ear cress)
 C/Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text_change 05-Oct-2004
 C/Accession: S30145; S34040; S36884
 R/Curien, G.; Dumas, R.; Douce, R.
 Plant Mol. Biol. 21, 717-722, 1993
 A/Title: Nucleotide sequence and characterization of a cDNA encoding the acetohydroxy ac
 A/Reference number: S30145; MUID:93192533; PMID:8448371
 A/Accession: S30145
 A/Molecule type: mRNA
 A/Residues: 1-591 <CUR>
 A/Cross-references: UNIPROT:Q05758; UNIPARC:UPI0000171F83; EMBL:X68150
 R/Dumas, R.
 submitted to the EMBL Data Library, July 1992
 A/Reference number: S34040
 A/Accession: S34040
 A/Molecule type: mRNA
 A/Residues: 1-284, 'R', 286-591 <DUM>
 A/Cross-references: UNIPARC:UPI000016DB78; EMBL:X68150; NID:g288062; PIDN:CAA48253.1; PI
 R/Dumas, R.; Curien, G.; DeRose, R.T.; Douce, R.
 Biochem. J. 294, 821-828, 1993
 A/Title: Branched-chain-amino-acid biosynthesis in plants: molecular cloning and charact
 s thaliana (thale cress).
 A/Reference number: S36884; MUID:93393563; PMID:8379936
 A/Accession: S36884
 A/Molecule type: DNA
 A/Residues: 1-578, 'A', 580-591 <DU2>
 A/Cross-references: UNIPARC:UPI0000000A7B; EMBL:X69880; NID:g402551; PIDN:CAA49506.1; PI
 C/Genetics:
 A/Genome: nuclear
 A/Introns: 99/3; 152/3; 159/3; 275/3; 315/1; 361/3; 417/3; 469/3
 C/Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase hom
 C/Keywords: chloroplast; isoleucine-valine biosynthesis; isomerase; oxidoreductase

F:1-67/Domain: transit peptide (chloroplast) #status predicted <TNP>
 F:68-591/Product: ketol-acid reductoisomerase #status predicted <MAT>
 F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.3%; Score 465; DB 1; Length 591;
 Best Local Similarity 27.2%; Pred. No. 2.3e-26;
 Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;
 QY 7 TKALRPLARQLATPAVQRTFVAASAVRASVAVKA-VAAPARQOVRGVKTMDFAGHKEE 65
 DB 44 SKLSRLT---ATVAGNGATGSSLAARWSSAVKAPVSLDFETSVFKKVKVSLAGVEEY 100

QY 66 VHERADWPAEKLLDYFNK-DTLALIGVSGQHGGGLNLRD-----NGLNIVGVKNGK 118
 DB 101 IVRGGRDLFLKHLDPDAFKGIQIGVIGWGSQGPAAQNLRDLSLVEAKSDIVVKGILRGSR 160
 QY 119 SWEDIAQDGVV-PGKNLFDVDEALSRGTIVNNLLSDAAQSTWPHIKPQITKGTLYFSH 177
 DB 161 SFPEARAGFTESGTLGDIWETIAGSDVLLISDAQAADNYEKIFSHMKPNLSILGLSH 220
 QY 178 GFSPVFKDLTKVEVPTDVLVAPKSGRTVRSFLRGR-----GINSSFAVYQDVTKG 232
 DB 221 GFLGLHQLSSGLDFPKNISVAVCPKMGPSVRLYVQKKEINGAGINAFVHQDVDR 280
 QY 233 AKKAVALGVAVGSGYLTYTFEYVSDLYGBRGCLMGGIHG----- 275
 DB 281 AADVAGWSVALGSPFTFATTLQEYRSDIFGERGILLGAVHGIVESLFRYRTENGMSD 340
 QY 276 ----- 275
 DB 341 LAYKNTVECTGTISRTISQTGMLAVVNSLSEBKKDFETAYSASFPCMEILYECYEDV 400
 QY 276 ----- 275
 DB 401 QSGSEIRSVVLGRFRFYKEKGLPAFPMGNIDQTRMKVGRVRSRPAAGDLGLPYPTAG 460
 QY 276 -----MFLAQEVLRLRERHSPSEA FNETVEBATOGLYPLIGHGMDWMDACSTTARRGAI 331
 DB 461 VYVALMAAQIEILRKKGHSYSEI NESVIESVDSLNPFMHARGVSFVMDNCSTTARLGSR 520
 QY 332 DWTPKF 337
 DB 521 KWAPRF 526

RESULT 11

T45681
 ketol-acid reductoisomerase - Arabidopsis thaliana

N/Alternate names: protein F14P22.200
 C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 04-Feb-2000 #sequence_revision 04-Feb-2000 #text_change 05-Oct-2004

C/Accession: T45681

R/D'Angelo, M.; Vezzi, A.; Modesto, D.; Pigazzi, M.; Valle, G.; Mewes, H.W.; Lemcke, K.;
 submitted to the Protein Sequence Database, January 2000

A/Reference number: Z23011

A/Accession: T45681

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-591 <DAN>

A/Cross-references: UNIPROT:Q05758; UNIPARC:UPI0000000A7B; EMBL:AL137082

A/Experimental source: cultivar Columbia; BAC clone F14P22

C/Genetics:

A/Map position: 3

A/Introns: 99/3; 130/3; 152/3; 159/3; 275/3; 315/1; 361/3; 417/3; 469/3

A/Note: F14P22.200

C/Superfamily: ketol-acid reductoisomerase, plant type; ketol-acid reductoisomerase homol

F:123-321/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 22.3%; Score 465; DB 2; Length 591;

Best Local Similarity 27.2%; Pred. No. 2.3e-26;

Matches 132; Conservative 68; Mismatches 128; Indels 158; Gaps 7;

QY 7 TKALRPLARQLATPAVQRTFVAASAVRASVAVKA-VAAPARQOVRGVKTMDFAGHKEE 65

Db 44 SKLSRST---ATVAGNGATGSSLAARMVSSSAVAPVSLDFTSVFKKESLAGYEY 100
Qy 66 VHERADWPAEKLIDYFKN-DTALIGYSGHGGQGLNLRD-----NGLNVIIVGRKNGK 118
Db 101 IVGGRDLFKHLDPAFKGIQKIGVIGWGSQPAQAQNLRDSUVEAKSDIVVKILGRKGR 160
Qy 119 SWEDAIQDQWV-FGKNLFDVDEAIRSGTIVMNLSDAAQSETWPHIKPQITKGTLYFSH 177
Db 161 SPEEARAAGFTBSGTLGDIWETIAGSDLVLLISDAAQADNVEKIFSHMKPNSILGLSH 220
Qy 178 GFSFVFKDLTKVEVPTDVIDVLVAPKSGRGTVRSLSFREG------GINSFAYVQDVTGK 232
Db 221 GFLHLGSLGGLDFPKNISVAVVCPKMGSGFVSRLYVQKGKEINGAGINASFVHQDVDR 280
Qy 233 AKEKAVAGVAVSGYLYETTFEKEVYSDLYGRGCLMGGIHG----- 275
Db 281 AADVALGWSVALGSPPTFATLLEQYRSDFIGERGILLGNVHGIVESLFRRYTENGMSD 340
Qy 276 ----- 275
Db 341 LAYKNTVECTITRTISTQGLAVVNSLSBEGKDFETAVSASFYPCWEILYECYEDV 400
Qy 276 ----- 275
Db 401 QSGSEIRSVVLAGRFRYEKGLPAFPMGNIDQTRMMKVGSRVRSKSPAGDLPLYPFTAG 460
Qy 276 ----MFLAQVEVLRERGHSPSEAFNETVEATOSLYPLICAHGMDWDFACSTTARRGAI 331
Db 461 VYVALMMAQIEILRKKGHSSEIINSESVIESVDLSNPFHEARGVSPWVNCSTIARLGR 520
Qy 332 DWTPKF 337
Db 521 KWAPRF 526
RESULT 12
C90204
ketol-acid reductoisomerase (ilvC-1) [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 05-Oct-2004
C:Accession: C90204
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, R.
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: C90204
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KUR>
A:Cross-references: UNIPROT:Q9UMX9; UNIPARC:UPI000012D50D; GB:AE006641; NID:g13813740; E
C:Genetics:
A:Gene: ilvC-1
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
Query Match 22.2%; Score 463; DB 2; Length 335;
Best Local Similarity 34.1%; Pred. No. 1.5e-26;
Matches 112; Conservative 55; Mismatches 115; Indels 46; Gaps 8;
Qy 78 LDYFKNDTLALIGYSGHGGQGLNLRDGLNVIIVGRKNGKSWEDAIQDGVPGKMLFDV 137
Db 15 LDLIKGRIAVLGYSGRAWAQNLRDGLNVIIVGLEREGKSWELAKSDGITP----LHT 70
Qy 138 DEAIRSGTIVMNLSDAAQSETW-PHIKPOITKGTLYFSHGSPVFKDLTKVEVPTDVID 196
Db 71 KDAVKDADIIIFLVPDWQRTLWLESVQPMKKGADLVFAHGNIHYK---LIDPPKSDS 127
Qy 197 VILVAPKSGRGTVRSLSFREGGINSSFAYVQDVTGKAKEKAVAGVAVGS--GYLYETTF 254
Db 128 VYMIAPKPGPTVREYKAGGVAPALVAHVQDVSGLTHKALAIKAGIGATRAGVPTTF 187

Qy 255 EKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEATOSLYPLIGANG 314
Db 188 KEETETDLFGEQVILVGGIMELMRAAFETLBEGYQPEVAYPETINE-LKMLVDLVYEXG 246
Qy 315 MDWMPDCASTTARRG-----AIDWTPFKDALKPVF 345
Db 247 ISGMLKAVSDTAKYGGMTVGKVIDESVRKRKMEALQRIKSGFAEWEVYGRGMPTVV 306
Qy 346 NNLVSDVKNGBDRK-----RSLEYNSQP 368
Db 307 NGL-SNVQNSLEEKIGNQLRDLVQKGP 333
RESULT 13
A96911
ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C:Accession: A96911
R;Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee,
J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96911
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-337 <KUR>
A:Cross-references: UNIPROT:Q97WV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1;
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC0091
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
Query Match 22.2%; Score 463; DB 2; Length 337;
Best Local Similarity 35.2%; Pred. No. 1.5e-26;
Matches 118; Conservative 62; Mismatches 135; Indels 20; Gaps 9;
Qy 64 EBVHERADWPAEKLIDYFKNDTLALIGYSGHGGQGLNLRDGLNVIIVGRKNGKSWEDA 123
Db 2 EELKYVYDEAD--LNYLKDKKIIAIFGSGQGHAAHNLKESGLNVIIVGLYDGSKSWYA 59
Qy 124 IQDGVPGKMLFDVDEAIRSGTIVMNLSDAAQSETW-PHIKPOITKGTLYFSHGFSVP 182
Db 60 EDYGF----EYVEADAVKQAQVVMILLPDEKQKQIYEASIKDNLDEGDALFFAHGFNIH 115
Qy 183 FKDLTKVEVPTDVIDVLVAPKSGRGTVRSLSFREGGINSSFAYVQDVTGKAKEKAVAGV 242
Db 116 YNQIVP---PRVDVIMTAPKGFHIVRRQYTEGGVPCLYAVHQDYTGKKEIALAYGK 172
Qy 243 AVG--SGLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 300
Db 173 GIGGTGGVMMNTTFKIEETETDLFGQAVLCGGICALINAGYDTLREAGYSAENAYFECFH 232
Qy 301 EATOSLYPLIGAHGMDWMPDCASTTARRG-AIDWTPFKDALKPVFNILYDSVKNGDERK 359
Db 233 E-MKMLVIDLWYRGGMKRYISIDTAEYGDYVVGVRNLINDNVRABEMKKVLTBIQDGTFAK 291
Qy 360 RSLEYN--SQPDYRERYAELEIRNLRIWRAKGR 392
Db 292 NWLLENQTCRPAFNARRIEADR----ETEKVGR 322
RESULT 14
K84032
ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession: C84032
R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioacceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 20.7895 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-2
Perfect score: 2071
Sequence: 1 MLRTQARLLCNSRVITAKR.....RNMEIWKVGEVRKLRPNQ 395

Scoring table: BIOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	1 A24709	ketol-acid reducto
2	1508.5	72.8	400	1 UC1428	ketol-acid reducto
3	1467.5	70.9	404	2 T40532	ketol-acid reducto
4	495	23.9	332	2 H75044	ketol-acid reducto
5	485.5	23.4	333	2 F70407	acetohydroxy acid
6	478	23.1	348	1 F64492	ketol-acid reducto
7	470	22.7	337	2 A96911	ketol-acid reducto
8	468	22.6	331	2 AC1694	ketol-acid reducto
9	468	22.6	335	2 C92024	ketol-acid reducto
10	468	22.6	336	2 D72362	ketol-acid reducto
11	465	22.5	331	2 AB1323	ketol-acid reducto
12	461	22.3	342	2 C69644	ketol-acid reducto
13	443.5	21.4	340	2 C84032	ketol-acid reducto
14	442	21.3	367	1 A47037	ketol-acid reducto
15	441.5	21.3	334	2 F89937	ketol-acid reducto
16	437	21.1	363	2 C75387	ketol-acid reducto
17	435.5	21.0	591	1 S30145	ketol-acid reducto
18	435.5	21.0	591	2 T45681	ketol-acid reducto
19	433.5	20.9	337	2 C81801	ketol-acid reducto
20	433.5	20.9	337	2 P81066	ketol-acid reducto
21	433.5	20.9	581	2 T06825	ketol-acid reducto
22	432.5	20.9	333	2 A69059	ketol-acid reducto
23	432	20.9	331	2 AD2095	ketol-acid reducto
24	431	20.8	340	2 C97922	ketol-acid reducto
25	428.5	20.7	336	2 G95051	ketol-acid reducto
26	421.5	20.4	332	2 H69497	ketol-acid reducto
27	397	19.2	595	1 S17180	ketol-acid reducto
28	394	19.0	340	2 B86778	ketol-acid reducto
29	389	18.8	366	2 B82634	ketol-acid reducto

30	385	18.6	340	2 G81411	ketol-acid reducto
31	372.5	18.0	344	1 S35140	probable ketol-aci
32	369	17.8	332	2 T35830	acetolactate synth
33	365	17.6	338	2 E83059	ketol-acid reducto
34	359.5	17.4	338	1 C48648	ketol-acid reducto
35	357	17.2	333	1 JC5166	ketol-acid reducto
36	352.5	17.0	339	2 AB3330	ketol-acid reducto
37	350.5	16.9	339	2 AE2824	ketol-acid reducto
38	350.5	16.9	339	2 D97602	hypothetical prote
39	339	16.4	491	1 ISECKR	ketol-acid reducto
40	339	16.4	491	2 D91217	ketol-acid reducto
41	339	16.4	491	2 E86063	ketol-acid reducto
42	336	16.2	333	2 D70855	probable ilvC prot
43	336	16.2	333	2 H87120	ketol-acid reducto
44	336	16.2	343	2 T45415	ketol-acid reducto
45	335	16.2	492	2 AG0473	ketol-acid reducto

ALIGNMENTS

RESULT 1
A24709
ketol-acid reductoisomerase (EC 1.1.1.86) ILV5 - yeast (Saccharomyces cerevisiae)
N:Alternate names: acetohydroxyacid reductoisomerase ILV5; protein L9638.7; protein YLR33
C:Species: Saccharomyces cerevisiae
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C:Accession: A24709, S51463
R:Peteren J.G.L.; Holmberg S.
M:Ketol-acid reductoisomerase, highly expressed.
A:Title: The ILV5 gene of Saccharomyces cerevisiae is highly expressed.
A:Reference number: A24709; MIMD:87117524; PMID:3027658
A:Accession: A24709
A:Molecule type: DNA
A:Residues: 1-395 <PST>
A:Cross-references: UNIPROT:P06168; UNIPARC:UPI000012D529; EMBL:X04969; NID:G3826; PIDN:C
R:Du, Z.
submitted to the EMBL Data Library, December 1994
A:Description: The sequence of S. cerevisiae cosmid 9638.
A:Reference number: S51459
A:Accession: S51463
A:Molecule type: DNA
A:Residues: 1-395 <DUZ>
A:Cross-references: UNIPARC:UPI000012D529; EMBL:U19102; NID:G609396; PIDN:AA867753.1; PII
C:Genetic:SGD
A:Gene: SGD:ILV5; MIPS:YLR355C
A:Cross-references: SGD:S0004347; MIPS:YLR355C
A:Map position: 12R
C:Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
F:81-267/Domain: ketol-acid reductoisomerase homology <KAR>
Query Match 100.0%; Score 2071; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.4e-147;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTQARLLCNSRVITAKRTPALATPAAYSPRAAFVPMITTRRLKQINFGTETV 60
Db 1 MLRTQARLLCNSRVITAKRTPALATPAAYSPRAAFVPMITTRRLKQINFGTETV 60
QY 61 YERADMPREKLDYFKNDTFALIGYSGQYGQGLNLNDGNIYIGVKGAGAKAIED 120
Db 61 YERADMPREKLDYFKNDTFALIGYSGQYGQGLNLNDGNIYIGVKGAGAKAIED 120
QY 121 GWVPGKULFTVEDAIKRGSYVMNLSDAQSFTWPAIKPLLTGKTLTFSHGSPVVKDL 180
Db 121 GWVPGKULFTVEDAIKRGSYVMNLSDAQSFTWPAIKPLLTGKTLTFSHGSPVVKDL 180
QY 181 THVEPPKDLVILVAPGSGRTVRSLEKRGINSYAANNVDTGKAHEKQALAAVIGS 240
Db 181 THVEPPKDLVILVAPGSGRTVRSLEKRGINSYAANNVDTGKAHEKQALAAVIGS 240
QY 241 GYVYQTLTFEREVNSDLVGBRGCLMGHGMFLAQYDVLRENGHSPBAFVETVETATQSL 300

Db 241 GYAYQTFFEEVNSDLVGERGCLMGIGHMFLAQYDLIRNGHSPSEAFMEVEEAQSL 300
QY 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETKRSLEFNS 360
Db 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETKRSLEFNS 360
QY 361 QPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395
Db 361 QPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395

RESULT 2

UC1428
ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa
N/Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase
C/Species: Neurospora crassa
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004
C/Accession: UC1428
R/Sista, H.; Bowman, B.
Gene 120, 115-118, 1992
A/Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-H
A/Reference number: UC1428; MUID:30103010; PMID:1398116
A/Accession: JCI428
A/Molecule type: DNA
A/Residues: 1-400 <SIS>
A/Cross-references: UNIPROT:P38674; UNIPARC:UP1000012D525; GB:M84189; NID:G168821; PIDN:
C/Genetics:
A:Gene: ilv-2
A:Map position: V
A/Intons: 68/1, 78/3, 170/3, 392/3
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F/87-273/Domin: ketol-acid reductoisomerase homology <KAR>

Query Match 72.8%; Score 1508.5; DB 1; Length 400;
Best Local Similarity 73.6%; Pred. No. 2.1e-105;
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;

QY 4 TQARLICSNRVITA--KRTF---ALATRAA---AYSPPARFVKMTTRGKQINFG 54
Db 7 TKLRPLARQLATPAPVQRRTFVAASAVRASVAVKAAARQOV-----RGVKTMDFA 60
QY 55 GTVETVYERADWPREKLDLDFKNDTFALIGYSGQYGGGGLNLDNGLNVITIGVKDGASW 114
Db 61 GHKEEYVERADWPREKLDLDFKNDTFALIGYSGQYGGGGLNLDNGLNVITIGVKDGASW 120
QY 115 KAIIEDGWVPGKULFTVEDAIKRGSYVMNLLSDAOSETWPAIKPLLTGKTLTFSGHFS 174
Db 121 EDALIDGWVPGKULFTVEDAIKRGSYVMNLLSDAOSETWPAIKPLLTGKTLTFSGHFS 180
QY 175 PVFKDLTHVEPPKDLVILVAPKSGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQAL 234
Db 181 PVFKDLTHVEPPKDLVILVAPKSGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQAL 240
QY 235 AVAIGSYVYQTTFFEEVNSDLVGERGCLMGIGHMFLAQYDLIRNGHSPSEAFMEVE 294
Db 241 GVAVGSYVYQTTFFEEVNSDLVGERGCLMGIGHMFLAQYDLIRNGHSPSEAFMEVE 300
QY 295 EAQOSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETK 354
Db 301 EAQOSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETK 360
QY 355 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 395
Db 361 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVYKRLRPENQ 399

RESULT 3
T40532
ketol-acid reductoisomerase (EC 1.1.1.86) [similarity] - fission yeast (Schizosaccharomy
C/Species: Schizosaccharomyces pombe
C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 05-Oct-2004

C/Accession: T40532; T43303; T42540
R/Purnille, B.; Goffeau, A.; Wood, V.; Lyne, M.H.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, May 1998
A/Reference number: Z21935
A/Accession: T40532
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-404 <PUR>
A/Cross-references: UNIPROT:P78827; UNIPARC:UP1000012D527; EMBL:AL023288; NID:G5832408; I
A/Experimental source: strain 972h-; cosmid c56F2
R/Kawakita, M.
submitted to the EMBL Data Library, December 1997
A/Description: S.pombe ILV5 homology.
A/Reference number: Z22407
A/Accession: T43303
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 262-404 <KAM>
A/Cross-references: UNIPARC:UP10000168765; EMBL:AB09603; NID:G2696653; PIDN:BA24000.1;
R/Yoshioka, S.; Kato, K.; Nakai, K.; Okayama, H.; Nojima, H.
DNA Res. 4, 363-369, 1997
A/Title: Identification of open reading frames in Schizosaccharomyces pombe cDNAs.
A/Reference number: Z17323; MUID:98162722; PMID:9501991
A/Accession: T42540
A/Status: Preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-37, 'R', 39-40, 'W', 42-91, 'S', 93-237, 'T', 239-274, 'P', 276-296, 'P', 298-393, 'G',
A/Cross-references: UNIPARC:UP1000016909E; EMBL:DB9175; NID:G1749557; PIDN:BA11837.1; P
A/Experimental source: strain PR745
C/Genetics:
A:Gene: SPDB:SPBC56F2.12
A:Map position: 2
A/Function:

C/Pathway: branched-chain amino acid biosynthesis
C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; oxidoreductase
F/88-274/Domin: ketol-acid reductoisomerase homology <KAR>

Query Match 70.9%; Score 1467.5; DB 2; Length 404;
Best Local Similarity 70.2%; Pred. No. 2.5e-102;
Matches 276; Conservative 48; Mismatches 64; Indels 5; Gaps 1;

QY 2 LRTQARLICSNRVITAKRTPALATRAAAYSPPARFVKMTTRGKQINFGTETVY 61
Db 14 LRTMSGR-----RLATRSMVMAKRTIAAPSMFPAPMTAPLMQTRGMRYMDFAGTRENW 68
QY 62 ERADWPREKLDLDFKNDTFALIGYSGQYGGGGLNLDNGLNVITIGVKDGASWKAIEDG 121
Db 69 ERADWPREKLDLDFKNDTFALIGYSGQYGGGGLNLDNGLNVITIGVKDGASWKAIEDG 128
QY 122 WVGKULFTVEDAIKRGSYVMNLLSDAOSETWPAIKPLLTGKTLTFSGHSPVFKDLT 181
Db 129 WVGKULFTVEDAIKRGSYVMNLLSDAOSETWPAIKPLLTGKTLTFSGHSPVFKDLT 188
QY 182 HVEPPKDLVILVAPKSGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQALAVISG 241
Db 189 KHPDPDVVILVAPKSGRTVRSLEFKRGINSYAVWMDVTGKAHEKAQALAVISG 248
QY 242 YVYQTTFFEEVNSDLVGERGCLMGIGHMFLAQYDLIRNGHSPSEAFMEVEEAQSLY 301
Db 249 YVYQTTFFEEVNSDLVGERGCLMGIGHMFLAQYDLIRNGHSPSEAFMEVEEAQSLY 308
QY 302 PLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETKRSLEFNSQ 361
Db 309 PLIGKGYMDYDACSTTARRGALDWYPIFKNALKEFVDLYSTNGTETKRSLEFNSQ 368
QY 362 PDYREKLEKELDTIRNMEIWKVGEVYKRLRPEN 394
Db 369 PDYREKLEKELDTIRNMEIWKVGEVYKRLRPEN 401

RESULT 4
H75044


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Oy      361 QPDYREKLEKELDTRINME---TWVGGEVRL 390
          ||      |: : | | ||||: ||:
Db      313 ---REKGFPHNALRLKEKHLTEKVGKEIRKM 342

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RESULT 7

ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum
C:Species: Clostridium acetobutylicum
C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004
C:Accession: A96911
R:Noiling, J.; Bretton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
J. Bacteriol. 183, 4823-4838, 2001
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing *Clostridium* Cid
A:Reference number: A96900; MUID:21359325; PMID:21359325
A:Accession: A96911
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-537 <KTR>
A:Cross-references: UNIPROT:Q97MW0, UNIPARC:UPI00000C9D5C, GB:AB001437, PTDN:AAK78076.1#
A:Experimental source: Clostridium acetobutylicum ATCC824
C:Genetics:
A:Gene: CAC091
Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase

Query Match	22.7%	Score 470;	DB 2;	Length 337;
Best Local Similarity	36.1%;	Pred. No. 1.1e-27;		
Matches 122;	Conservative	58;	Mismatches 130;	Indels 28;
			Gaps	10;

QY 72 LDYFKNDTFALIGYGSGYGGLNLRDNGLNVIIGVRKDGA\$WKAIEDGWVPK\$NLFVV 131

Db 14 LNYLKDKKIAIIGFGSGHAHALNKESGINVIGLYDGSKSMKVAEDYGF---EYVEY 69

QY 132 EDAIKRGSYMNLSDAQSETWPA-IKPLLTGKTLYFSHGSPVFKDLTHEPPKDL 190

Db 70 ADAAVKQAQVVMILLPDEKQKIYEASIKDNLDEGDALFAHGFNIHYNQIV--PPKAVD 126

191 VILVAPKSGRTVRSLEKEGRINSSYAVWNDVTGAHEKAQALAVAIG--SGYVYQTTF 248

DB 127 VLMIAKPGFHI VRRQYTEGGVPCLYAVHODYTGKGEIALAYGKGIGGTGGVMTTF 186

245 ENEVNSDPIGERGCLMGIGHMF LAQI DVLRNGHSPSEAFNEIVEEAIQSLPYPLIGKYG 308

23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 105

[illegible]

0 2 4 6 8 10 12 14 16 18 20 22 24 26 28 30 32 34 36 38 40 42 44 46 48 50 52 54 56 58 60 62 64 66 68 70 72 74 76 78 80 82 84 86 88 90 92 94 96 98 100

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304 ENABPRD -- BPRF/CVBI BOMMCWTNPRDCTR 337

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RESULT 2

ketol-acid reductoisomerase (acetohydroxy-acid isomeroeductase) homolog ilvc [imported]
C/Species: *Listeria innocua*
C/Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C/Accession: AC1694
R/Glasser, P.; Frangoul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloecher
D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duseurget, O.; Entian, K.D.; Feihl, H.
Science 294, 849-852, 2001
D.; Jones, L.M.; Karet, U.
A/Authors: Kretz, J.; Kuhn, M.; Kunst, F.; Kurapkac, G.; Madueno, E.; Maltournam, A.; Ma
ok, C.; Schluerer, T.; Simoes, N.; Tierzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A./Title: Comparative genomics of *Listeria* species.
A/Reference number: AB1077, MUID:2153729; PMID:11679669
A/Accession: AC1694
A/Status: preliminary
A/Molecule type: DNA

A:Residues: 1-331 <Gla>
A:Cross-references: UNIPARC:UPI000000CCT59, GB:AL552022, PIDN:CAC97323.1, PTD:516414607, C
A:Experimental source: strain Clp11262

A;Gene: ilvC

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Best Local Similarity 37.3%; Pred. NO: 1.6e-27;
Matches 125: Conservative 60: Mismatches 118. Indels 32. Gaps 13.

QY 73 DYFKND-----TFALIGYSOGYGGLNLRDNGLNVTIGVRKDGASWKAIEDGWVPCKN 127

Db 8 DAVKNNAL^{EG}KT^{AV}IG^{YG}SQ^{GH}AH^{SQ}NLRD^{NG}NN^{VI}IG^{IR}-EGKSAESARNDGF-----D 62

128 LFTVEDAIKGSVNNLLSDAQSETP-AIKPLLTKGKTLFESHGSPVFKDLTHVEPP 186

Db 63 VYSVSEAEKADVIMILLPDETQGETYENEIKPNLKAGNALVFAHGFNIHF-DV--INPP 119

187 KDLDVILVAPKGSGRVRSLFKEGRGINSSYAVNBDVTGKAHEKAQALAVAIGS--GYVY 244

DB 120 SVDVFLVAPKGPGLVRRITVEGGAVPSLEAIYQDAIGNARDIALSYAKGIIGAIRAGVI 179

[illegible]

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This image shows a vertical strip of a film negative. It contains various horizontal lines and patterns of dots, which are likely representations of film frames or a series of images. The patterns include solid lines, dashed lines, and clusters of dots, suggesting different visual elements or data points captured in the film.

[illegible]

295 KN-GEKEFHRMRKE---OGHOTEKVGAET;REMP 325

RESULT 9

ketol-acid reductoisomerase [ilvc-1] [imported] - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C:Date: 24-May-2001 #sequence revision 24-May-2001 #text_change 05-Oct-2004
C:Accession: G90204
R:Shu, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-Wong, J.; Jeffries, A.C.; Kozera, C.U.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P.; Barrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A89139
A:Accession: G90204
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-335 <KUR>
A:Cross-references: UNIPROT:Q9UWX9, UNIPARC:UPI000012D50D, GB:AE006641, P1C:Genetics:
A:Gene: ilvc-1
A:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type, ketol-acid reductoisom

Query Match 22.6%; Score 468; DB 2; Length 335;

Matches 112; Conservative 65; Mismatches 129; Indels 20; Gaps 8;

72 LDYFKNDTFALIGYGSQGYGGGLNRDNGLNVIIGVRKDGASWKALIEDGWPgKNLFTV 131

DB 15 LDDLKGRKIAVLGYGSQGRWAQNLRKDSGLNVVGLEREGKSWELAKSDGIIPE---LHT /0

102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 1054 1055 1056 1057 1058 1059 1060 1061 1062 1063 1064 1065 1066 1067 1068 1069 1070 1071 1072 1073 1074 1075 1076 1077 1078 1079 1080 1081 1082 1083 1084 1085 1086 1087 1088 1089 1090 1091 1092 1093 1094 1095 1096 1097 1098 1099 11

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QY 249 EREVNNDLYGKRGCMGHIHGMFLAQVDVLRNGHSPSEAFNVEATQSLYPLIGKYG 308
 DB 188 KEETETDLEGEVIVILYGGIMELMRAAFETLVBEQOPEVAYETITNE-LKMLVDLYVRKG 246
 QY 309 MDVWDACSTTARRGALDWYP-IFKNALKPVFODIYESTKNGETKRSLEFNSQDYREK 367
 DB 247 ISGMLKAVSDIKYGMVYGVKVIDESVRKMKELQRIKSKFAEWEV-----EYGRG 301
 QY 368 LE---KEIDTIRNMEIWKVGEVRL 390
 DB 302 MPTVNGLSNVGNLSLEKIGNQLRL 327
 RESULT 10
 D72362
 ketol-acid reductoisomerase - Thermotoga maritima (strain MSB8)
 C:Species: Thermotoga maritima
 C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 05-Oct-2004
 C:Accession: D72362
 R:Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey
 Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
 C.M.
 Nature 399, 323-329, 1999
 A:Title: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
 A:Reference number: A72200; MUID:99287316; PMID:10360571
 A:Accession: D72362
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-336 <ARN>
 A:Cross-references: UNIPROT:Q9WZ20; UNIPARC:UPI000012D560; GB:AE001730; GB:AE000512; NID
 A:Experimental source: strain MSB8
 C:Gene(s):
 A:Gene: TM0550
 C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
 F:21-203/Domain: ketol-acid reductoisomerase homology <KAR>
 Query Match 22.6%; Score 468; DB 2; Length 336;
 Best Local Similarity 35.6%; Pred. No. 1.6e-27;
 Matches 117; Conservative 66; Mismatches 124; Indels 22; Gaps 8;
 QY 72 LDYFNDPFLALIGYSGYGGGLNRDNGLNITIGVRKDGASWKAIEDGVPKGLTFV 131
 DB 12 LNLIDKKIATIGYSGQHAAHLNKKDGLNVVGLRSGSKWKAEEQ---GLTVKTI 67
 QY 132 EDATKRGSVNMLSDAQSFTWPA-IRPLLTGKTLVFSHGSVPFVDLTHVEPKDLD 190
 DB 68 BEAAKEADITIMLPDEHOPETLYKYIEKHILTEGMLFAHGFENHYHII---PPKVD 124
 QY 191 VILVAPKSGRTVRSILFKRGINSYAVMNDVTGSKAHEKAQALVAIG--SGVYVQTF 248
 DB 125 VTMIAFKSPGHIVREYVBEGRVPLVAVYQDYTKADIALAYAKGIGVTRAGYIETTF 184
 QY 249 EREVNNDLYGKRGCMGHIHGMFLAQVDVLRNGHSPSEAFNVEATQSLYPLIGKYG 308
 DB 188 KEETETDLEGEVIVILYGGIMELMRAAFETLVBEQOPEVAYETITNE-LKMLVDLYVRKG 246
 QY 309 MDVWDACSTTARRGALDWYP-IFKNALKPVFODIYESTKNGETKRSLEFNSQDYREK 367
 DB 247 ISGMLKAVSDIKYGMVYGVKVIDESVRKMKELQRIKSKFAEWEV-----EYGRG 301
 QY 368 LE---KEIDTIRNMEIWKVGEVRL 390
 DB 302 MPTVNGLSNVGNLSLEKIGNQLRL 327
 RESULT 11
 AB1323
 ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]
 C:Species: Listeria monocytogenes
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
 C:Accession: AB1323
 R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker
 ; Dominguez-Bernal, G.; Duclaud, E.; Durand, L.; Dussange, O.; Entian, K.D.; Fsihi, H.

D.; Jones, L.M.; Karst, U.
 Science 294, 849-852, 2001
 A:Authors: Kretz, J.; Kunz, M.; Kunz, F.; Kurapak, G.; Madueno, E.; Maitournam, A.; Ma
 ok, C.; Schluter, T.; Simoes, N.; Tiller, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
 A:Title: Comparative genomics of *Listeria* species
 A:Reference number: AB1077; MUID:21537279; PMID:11679669
 A:Accession: AB1323
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-331 <GLA>
 A:Cross-references: UNIPARC:UPI0000054F6; GB:NC_003210; PIDN:CAD00064.1; PID:G16411439;
 A:Experimental source: strain ESD-e
 C:Gene(s):
 A:Gene: ilvC
 C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductois
 Query Match 22.5%; Score 465; DB 2; Length 331;
 Best Local Similarity 37.3%; Pred. No. 2.6e-27;
 Matches 125; Conservative 59; Mismatches 119; Indels 32; Gaps 13;
 QY 73 DYFND-----TFALIGYSGYGGGLNRDNGLNITIGVRKDGASWKAIEDGVPKGN 127
 DB 8 DAVKNNALGKTVAVITGYSGQHAAHLNKKDGLNVVGLRSGSKWKAEEQ---D 62
 QY 128 LFTVEDALIKRGSYVNLSDAQSFTWPA-IRPLLTGKTLVFSHGSVPFVDLTHVEPP 186
 DB 63 VYVSEADKADKADVIMILPDEHOPETLYKYIEKHILTEGMLFAHGFENHYHII---D-V-INP 119
 QY 187 KDVLVILVAPKSGRTVRSILFKRGINSYAVMNDVTGSKAHEKAQALVAIGS--GYV 244
 DB 120 SDVVFVLPAPKSPGHIVREYVBEGRVPLVAVYQDYTKADIALAYAKGIGVTRAGVI 179
 QY 245 OTTEREVNNDLYGKRGCMGHIHGMFLAQVDVLRNGHSPSEAFNVEATQSLYPLI 304
 DB 180 KEETETDLEGEVIVILYGGIMELMRAAFETLVBEQOPEVAYETITNE-LKMLVDLYVRKG 246
 QY 309 MDVWDACSTTARRGALDWYP-IFKNALKPVFODIYESTKNGETKRSLEFNSQDYREK 367
 DB 247 ISGMLKAVSDIKYGMVYGVKVIDESVRKMKELQRIKSKFAEWEV-----EYGRG 301
 QY 368 LE---KEIDTIRNMEIWKVGEVRL 390
 DB 302 MPTVNGLSNVGNLSLEKIGNQLRL 327
 RESULT 12
 C69644
 ketol-acid reductoisomerase ilvC - *Bacillus subtilis*
 C:Species: *Bacillus subtilis*
 C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
 C:Accession: C69644
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertek
 C.; Bron, S.; Brulliet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Gallizzi, A.; Gall
 iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holzapfel, S.; Hosono, S.; Hullo, M.F.;
 Koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidis, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
 Y. M.; Ogawa, K.; Ogiwara, A.; Oudegaa, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portet
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeter, R.; Scofield, F.; Sekiguchi, J.; Sekowska, A.; Ser
 akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida,
 A:Authors: Yoshikawa, H.F.; Zimstein, E.; Yoshikawa, H.; Zimstein, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: C69644
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-342 <KNA>
 A:Cross-references: UNIPROT:P37253; UNIPARC:UPI0000038DEF; GB:Z59118; GB:AL009126; NID:94
 A:Experimental source: strain 168

QY 386 EVRKL 390
DB 356 DLRAM 360

RESULT 15

89997
alpha-keto-beta-hydroxyacyl reductoisomerase [imported] - Staphylococcus aureus (strain
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 05-Oct-2004
C:Accession: F89997
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89997
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-334 <KUR>
A:Cross-references: UNIPARC:UPI00000D7826; GB:BA000018; PID:g13701851; PIDN:BA843143.1;
A:Experimental source: strain N315
C:Genetics:
A:Gene: ilvC
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom

Query Match 21.3%; Score 441.5; DB 2; Length 334;

Best local similarity 34.1%; Pred. No. 1.5e-25;
Matches 118; Conservative 68; Mismatches 125; Indels 35; Gaps 13;

QY 59 TVYERADMPREKLDYFKNDFPAGIGSGOGGGLNRDNGLANVIGVRKOGASWKAII 118
DB 3 TVY-----YDQVKTDLAQKIAVGVGSGQHAAHAKNLKNGYDVVIGIR-PGRSFDKAK 57
QY 119 EDGAVGKMLFTVEDAIRGSYVNNLSDAAQSETW-AIKPLTKGKTLVSHGSPFV 177
DB 58 EDGF----DVFPVAEAVKQADIVIMVLPDEIQGDVYKNEIBENLEKHNAIAFAGFNTHF 113
QY 178 KDLTVPEPKDLDTLVLPKSGGRTVRSLPKEGRGINSYAVMNDVTGAHKAQALVA 237
DB 114 --GVIQPPADVDFLVPKPGHLYRRTFVEGSAVPSLFGIQDASQARNIALSYAKG 170
QY 238 IGS--GYVYQTFPEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVTVEB 295
DB 171 IGATPAGVIERTFKEETETDLFGEQAVLCGVSKLIQSGFETLVAGYQPELAIYFEVLHE 230
QY 296 ATQSLYPLIGKXMDYWDACSTTARAGALPW-----PIFKNALKPVFDLYESTKN 348
DB 231 -MKLIVDLMEGGMENVYSISNTAFEG--DYVSGPRVITPDVKENMKAVLTLDI----QN 283
QY 349 GTETKRSLEFNSQPYRE--KLEKELDTIRNMEIKVQKEVRKLAP 392
DB 284 GNFSNRFLIEDNKN-GFKEFYKLRBEQ--HGHIKEKVGRELRKEMW 325

Search completed: March 22, 2006, 15:34:33
Job time : 21.7895 secs

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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 115.529 Seconds
(without alignments)
1528.885 Million cell updates/sec

Title: US-10-797-248A-1
Perfect score: 2094
Sequence: 1 MSARGFSKALPMPARQLATP.....EIMRAGKAVRSLRPENQKQK 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq21.*
1: Geneseq21980s.*
2: Geneseq21990s.*
3: Geneseq22000s.*
4: Geneseq22001s.*
5: Geneseq22002s.*
6: Geneseq22003as.*
7: Geneseq22003bs.*
8: Geneseq22004s.*
9: Geneseq22005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2094	100.0	402	6	ABR64303
2	2081	99.4	400	6	ABR64306
3	2081	99.4	400	9	ADVL16807
4	1856	88.6	400	6	ABR64305
5	1671	79.8	403	9	ADVL16810
6	1668	79.7	396	6	ABJ26477
7	1668	79.7	508	6	ABJ26502
8	1634	78.0	388	6	ABJ25902
9	1634	78.0	500	6	ABJ25877
10	1526.5	72.9	400	4	AAU15089
11	1526.5	72.9	400	5	ABP71238
12	1503	71.8	395	6	ABR64304
13	1503	71.8	395	7	ADK64188
14	1421.5	67.9	409	7	ADK70124
15	1100.5	52.6	347	6	ABU20976
16	490	23.4	342	4	AAU01250
17	475	22.7	331	5	ABBA48168
18	475	22.7	331	6	ABU32456
19	473	22.6	332	4	AAB96356
20	472	22.5	337	6	ABU24174
21	469.5	22.4	336	6	ABU18526
22	468	22.3	579	2	AAZ26183
23	468	22.3	579	2	AAZ26180
24	468	22.3	585	8	ADX93651

25	468	22.3	586	8	ADX88429	Adx88429 Plant ful
26	468	22.3	588	8	ADY07198	Ady07198 Plant ful
27	468	22.3	590	8	ADY07344	Ady07344 Plant ful
28	468	22.3	590	8	ADY77584	Ady77584 Plant ful
29	467	22.3	579	3	AAG35210	Ag35210 Zea mays
30	467	22.3	596	3	AAG35209	Ag35209 Zea mays
31	462.5	22.1	340	4	AAU37780	Aau37780 Streptoco
32	462.5	22.1	340	4	AAU38003	Aau38003 Streptoco
33	462.5	22.1	340	6	ABU00804	Abu00804 S. pneumo
34	462.5	22.1	340	6	ABU45897	Abu45897 protein e
35	462.5	22.1	340	8	ADK47367	Adk47367 Streptoco
36	462.5	22.1	351	8	ADR94886	Adr94886 Novel S.
37	462.5	22.1	351	8	AEA58756	Aea58756 Streptoco
38	462	22.1	581	9	ADY61069	Ady61069 Abiotic s
39	461.5	22.0	326	7	ADM26226	Adm26226 Hyperther
40	458	21.9	571	8	ADY04361	Ady04361 Plant ful
41	457	21.8	568	8	ADY07450	Ady07450 Plant ful
42	457	21.8	578	8	ADY92449	Ady92449 Plant ful
43	457	21.8	626	8	ADY07435	Ady07435 Plant ful
44	452	21.6	586	2	AAZ26182	Aaz26182 Soybean a
45	451.5	21.6	334	4	AAG81458	Aag81458 S. epider

ALIGNMENTS

RESULT 1

ABR64303
ID ABR64303 standard; protein; 402 AA.
XX
AC ABR64303;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductase #1.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Magnaporthe grisea.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
XX potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
XX isomeroreductase.
XX Claim 2; Fig 1; 66pp; French.
XX The present invention relates to a method for controlling fungal disease
XX in crops by applying an inhibitor (I) of acetohydroxyacid
XX isomeroreductase. (I) are used for curative or preventative treatment of
XX a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
XX rape. The present sequence is an acetohydroxyacid isomeroreductase, used
XX to illustrate the invention
SQ Sequence 402 AA;

Query Match 100.0%; Score 2094; DB 6; Length 402;
Best Local Similarity 100.0%; Pred. No. 1.4e-191;
Matches 402; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MSARGFSKALRPNARQLATPAVQRRSFVAASMWVRATRKAAVAPTQQOIRGVKTMDFAGH	60
Db	1	MSARGFSKALRPNARQLATPAVQRRSFVAASMWVRATRKAAVAPTQQOIRGVKTMDFAGH	60
Qy	61	KEQWVERADWPKEKLLLEYFKDDTLALIGVSGQHGGQGLNRDNGLNVIIGVRKDGKSWKD	120
Db	61	KEQWVERADWPKEKLLLEYFKDDTLALIGVSGQHGGQGLNRDNGLNVIIGVRKDGKSWKD	120
Qy	121	AVDQGWVPGKNLFEVDEAISRGTIVMNLISDAAQSETWPALKPQITKGKTLYFSHGFSVP	180
Db	121	AVDQGWVPGKNLFEVDEAISRGTIVMNLISDAAQSETWPALKPQITKGKTLYFSHGFSVP	180
Qy	181	FKDLTKVEVPTDVIDILCAPKGSGETVRSLSFRREGINSFPAVQDVTGSAEKAIALGV	240
Db	181	FKDLTKVEVPTDVIDILCAPKGSGETVRSLSFRREGINSFPAVQDVTGSAEKAIALGV	240
Qy	241	AIGSGYLKTKTTEKEVYSDLYGERCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA	300
Db	241	AIGSGYLKTKTTEKEVYSDLYGERCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVEEA	300
Qy	301	TQSLYPLIGANGMDWMYEACSTTARRGAIDWSRPFKDALKVFNQLYDSVKDGSQTSRSL	360
Db	301	TQSLYPLIGANGMDWMYEACSTTARRGAIDWSRPFKDALKVFNQLYDSVKDGSQTSRSL	360
Qy	361	DYNSQPDYREKYEAEEMBEIRNLEIWRAGKAVRSRLENQOK	420
Db	361	DYNSQPDYREKYEAEEMBEIRNLEIWRAGKAVRSRLENQOK	420
RESULT 2			
ABR64306			
ID	ABR64306 standard; protein; 400 AA.		
AC	ABR64306;		
AC	16-SEP-2003 (first entry)		
DT	Acetohydroxyacid isomeroreductas #2.		
DE	Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.		
KW	Magnaporthe grisea.		
OS	FR2829363-A1.		
PN	14-MAR-2003.		
XX	10-SEP-2001; 2001FR-00011689.		
XX	10-SEP-2001; 2001FR-00011689.		
XX	(AVET) AVENTIS CROPS SCIENCE SA.		
PA	Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;		
PI	WPI; 2003-405775/39.		
DR	N-PSDB; ACC80185, ACC80186.		
XX	Treatment of crops, useful for controlling fungi on, e.g. cereals,		
PT	potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid		
PT	isomeroreductase.		
XX	Disclosure; Page 57-58; 66pp; French.		
CC	The present invention relates to a method for controlling fungal disease		
CC	in crops by applying an inhibitor (I) of acetohydroxyacid		
CC	isomeroreductase. (II) are used for curative or preventative treatment of		
CC	a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or		
CC	rape. The present sequence is an acetohydroxyacid isomeroreductase, used		
CC	to illustrate the invention		
XX	SQ Sequence 400 AA;		

XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (Ocrase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting Ocrase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are:
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
 CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
 XX
 SQ Sequence 400 AA;

Query Match 99.4%; Score 2081; DB 9; Length 400;
 Best Local Similarity 99.8%; Pred. No. 2.5e-130;
 Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRATRKAAVAPTOQQOIRGVKTMDFAGH 60
 DB 1 MSARGFSKALRPMARQLATPAVQRRTFVAASSMVRATRKAAVAPTOQQOIRGVKTMDFAGH 60
 QY 61 KEQWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSWKD 120
 DB 61 KEQWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSWKD 120
 QY 121 AVQDQGWPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSGHGFSPV 180
 DB 121 AVQDQGWPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSGHGFSPV 180
 QY 181 FKDLTKVEPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEKAIALGV 240
 DB 181 FKDLTKVEPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEKAIALGV 240
 QY 241 AIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVEE 300
 DB 241 AIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVEE 300
 QY 301 TQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGETQSL 360
 DB 301 TQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGETQSL 360
 QY 361 DYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400
 DB 361 DYNQSDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400

RESULT 4
 ABR64305
 ID ABR64305 standard; protein; 400 AA.
 XX
 AC ABR64305;
 XX
 DT 16-SEP-2003 (first entry)
 XX
 DE Acetohydroxyacid isomeroreductase.
 XX
 XX Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
 XX
 XX Neurospora crassa.
 XX
 XX FR2829363-A1.
 XX
 XX 14-MAR-2003.
 XX
 XX 10-SEP-2001; 2001FR-00011689.

XX 10-SEP-2001; 2001FR-00011689.
 PR (AVET) AVENTIS CROPS SCIENCE SA.
 XX
 PA Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
 XX
 PI WPI; 2003-405775/39.
 XX
 DR Treatment of crops, useful for controlling fungi on, e.g. cereals,
 XX potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroreductase.
 PT
 XX Claim 2; Fig 1; 66pp; French.
 PS
 XX The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (I) of acetohydroxyacid
 CC isomeroreductase. (I) are used for curative or preventative treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
 CC to illustrate the invention
 XX
 SQ Sequence 400 AA;

Query Match 88.6%; Score 1856; DB 6; Length 400;
 Best Local Similarity 86.8%; Pred. No. 9.6e-169;
 Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASSMVRAT--RKAAPVTOQQOIRGVKTMDFEA 58
 DB 1 MAARNCTKALRPLARQLATPAVQRRTFVAASAVRASVAVKAAVAPARQVGRVKTMDFA 60
 QY 59 GHKEQWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSW 118
 DB 61 GHKEQWERADWPKEKLEFFKDDTLALIGYSGQGHGQGLNLDNGLNVIIGVRKDGKSW 120
 QY 119 KDAVQDQGWPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSGHGF 178
 DB 121 EDAIQDQGWPGKNLFEVDEAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSGHGF 180
 QY 179 PVFKDLTKVEPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEKAIAL 238
 DB 181 PVFKDLTKVEPTDVIILCAPKSGRTVRSIFREGGINSSFAVYQDVTGAEKAIAL 240
 QY 239 GVAIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVE 298
 DB 241 GVAIGSGYLYKTTFFKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNETVE 300
 QY 299 EATQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGETQSL 358
 DB 301 EATQSLYPLIGANGMDMYEACSTTARRGAIDWSPRFKDALKPVFNQLYDSVKDGETQSL 360
 QY 359 SLDYNSQDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400
 DB 361 SLDYNSQDPYREKYAEEMEEIRNLEIWRAGKAVRSIRPENQK 400

RESULT 5
 ADV16810
 ID ADV16810 standard; protein; 403 AA.
 XX
 AC ADV16810;
 XX
 DT 24-FEB-2005 (first entry)
 XX
 DE M graminicola ketol-acid reductoisomerase KAP1 seqid 9.
 XX
 XX substrate inhibition; antibiotic; gene disruption;
 KW ketol-acid reductoisomerase; KAP1; enzyme.
 XX
 OS Mycosphaerella graminicola.
 XX
 PN WO2004104176-A2.

XX 02-DEC-2004.
XX 17-MAY-2004; 2004WO-US015404.
XX 15-MAY-2003; 2003US-0470947P.
XX 19-MAY-2003; 2003US-0471615P.
XX 21-MAY-2003; 2003US-0472242P.
XX (PARA-) PARADIGM GENETICS INC.
XX Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
PI Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;
PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
XX WPI; 2005-021202/02.
DR N-PSDB; ADV16802, ADV16808, ADV16809.
XX
XX Identifying a test compound as a candidate for an antibiotic comprises
PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
PT with a test compound.
XX
XX Claim 50; SEQ ID NO 9; 179pp; English.
XX
XX The invention describes a method of identifying a test compound as a
CC candidate for an antibiotic comprising contacting ornithine
CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
CC or fungal pathogenicity-conferring gene with a test compound. The method
CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
CC ; and detecting the presence or absence of binding between the test
CC compound and the polypeptide or gene, where binding indicates that the
CC test compound is a candidate for an antibiotic. Also described are: an
CC isolated nucleic acid comprising a nucleotide sequence encoding a
CC polypeptide having at least 50% sequence identity to, or having at least
CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
CC polypeptide consisting essentially of the amino acid sequence of 400, 403
CC or 469 amino acids. The methods are useful for identifying inhibitors of
CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
CC pathogenicity-conferring gene as antibiotics. This is the amino acid
CC sequence of *Mycosphaerella graminicola* ketol-acid reductoisomerase KAR1.
XX
SQ Sequence 403 AA;

Query Match 79.8%; Score 1671; DB 9; Length 403;
Best Local Similarity 78.4%; Pred. No. 5.4e-151;
Matches 315; Conservative 40; Mismatches 43; Indels 4; Gaps 1;
1 MSARGFSKALRPMARQLATPAVORRSGFVAASSMVRAT---RKAAVAPTOQQIIRGVKTM 56
1 MASNATRALRASLRQLKAPQVQRGFVAANRPSLVPQAQVTSFVQVRGAKTV 60
57 FAGHKSQWVERADWPKEKLEYPKDDTLALIGYSGHGGQGLNLDNGLNVIIGVRKDGK 116
61 FAGDEKVFERDDWPKEKLEYPKDDTLALIGYSGHGGQGLNLDNGLNVIIGVRKGA 120
117 SWKDAVDQGWVPGKILFEVDEAISRGTIVMNLISDAQSETWPAKLPQITKGTLYFSHG 176
121 SWKEAGDGWGEKGNLFDIDTAIGKGTIIMNLSDAQSETWPHIKPMLTKGTLYFSHG 180
177 FSPVFKDLTKVEYPTDVIDLCAPKSGRTVRSFLFREGINSFSAVYQDVGTGEAEKAI 236
181 FSPVFKDQTKVEYPTDVIDLVAPKSGRTVRLFKREGINSIIAFQDVTGKAEKAI 240
237 ALGVAIGSGYLYTKTEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHGSPSEAFNET 296
241 ALGVAIGSGYMYTKTEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHGSPSEAFNET 300
297 VEATOSLYPLICANGMDMYEACSTTARRGATDWSPRFKDALKPVFNQLYDSVKDGET 356
301 VEATOSLYPLIKNGMDMYEACSTTARRGATDWSKRFKTLKPVFELYDSVKGTET 360

OY 357 ORSLDYNQSDYREKYAEEMERINLEIWRACKAVRSLRPN 398
DB 361 QRTMEYAGKDYREAFKEMERINLEIWRACKAVRSLRPN 402
RESULT 6
ABJ26477
ID ABJ26477 standard; protein; 396 AA.
XX AC ABJ26477;
XX DT 16-APR-2003 (first entry)
XX DE Aspergillus fumigatus essential gene protein #1135.
XX KW Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection;
KW cancer; contamination; biofilm; antibody; immune response.
XX OS *Aspergillus fumigatus*.
XX PN WO200286090-A2.
XX PD 31-OCT-2002.
XX PF 23-APR-2002; 2002WO-US013142.
XX PR 23-APR-2001; 2001US-0285697P.
XX PR 27-APR-2001; 2001US-0287066P.
XX PR 05-JUN-2001; 2001US-0295890P.
XX PR 09-JUL-2001; 2001US-0303899P.
XX PR 31-AUG-2001; 2001US-0316362P.
XX PA (ELIT-) ELITRA PHARM INC.
XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
XX WPI; 2003-093124/08.
XX PT New purified or isolated nucleic acids of essential genes of *Aspergillus*
PT *fumigatus*, useful for treating or preventing infections by *A. fumigatus*,
PT or for treating a non-infectious disease in a subject e.g. cancer.
XX PS Disclosure; Page; 175pp; English.
XX
XX The invention relates to novel purified or isolated nucleic acids of
CC essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of
CC the invention are used to treat or prevent infections by a pathogenic
CC organism such as *A. fumigatus*, to treat a non-infectious disease in a
CC subject (e.g. cancer), to prevent or contain contamination of an object
CC by *A. fumigatus*, or to prevent or inhibit formation on a surface of a
CC biofilm comprising *A. fumigatus*. The polynucleotides are useful for
CC expressing recombinant protein for characterisation, screening or
CC therapeutic use, as markers for host tissues in which the pathogenic
CC organisms invade or reside, for comparing with the DNA sequence of *A.*
CC *fumigatus* to identify duplicated genes or paralogues having the same or
CC similar biochemical activity and/or function, for comparing with DNA
CC sequences of other related or distant pathogenic organisms to identify
CC potential orthologous essential or virulence genes, for selecting and
CC making oligomers for attachment to a nucleic acid array for examination
CC of expression patterns, for raising anti-protein antibodies, as an
CC antigen to raise anti-DNA antibodies or to elicit another immune
CC response, and for identifying polynucleotides encoding the other protein
CC with which binding occurs or to identify inhibitors of the binding
CC interaction. The polypeptides may be used to raise antibodies or to
CC elicit immune response, as a reagent in assays designed to quantitatively
CC determine levels of the protein in biological fluids, as a marker for
CC host tissues in which pathogenic organism invade or reside, and to
CC isolate correlative receptors or ligands in the case or virulence
CC factors. This sequence represents a protein of one of the essential genes
CC of *Aspergillus fumigatus* of the invention
XX
SQ Sequence 396 AA;

Query Match 79.7%; Score 1668; DB 6; Length 396;
 Best Local Similarity 79.1%; Pred. No. 1e-150;
 Matches 318; Conservative 42; Mismatches 34; Indels 8; Gaps 4;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASMSVRATRKAA--VAPTOOQIRGVKTMDF 58
 1 MASRGLPRALR-LAR-VAAP-----RTVISALPPALAKAATRVAASTAPRGVKTITAF 54

QY 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGKSW 118
 55 DSKETVYERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGASW 114

QY 119 KDAVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPAKQITKGTLYFSHGFS 178
 115 KEAQDQWIPGKNLFDLTVAVQKGTIVMNLSDAAQSETWPLKPLITKGTLYFSHGFS 174

QY 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSLFREGRGINSFVAYQDVTGEAEKAI 238
 175 PVFKELTKVDVDPKDVILVAPKSGRTVRSLFREGRGINSFVAYQDVTGEAEKAI 234

QY 239 GVAIGSGVLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 235 GVAIGSGVLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 294

QY 299 EATQSLYPLICANGMDWMYACSTTARRGAIDMSRPFKDALKPVENQLYDSVKGDSGTOR 358
 295 EATQSLYPLICANGMDWMYACSTTARRGAIDMSRPFKDALKPVENQLYDSVKGDSGTOR 354

QY 359 SLDYNQSDPYREKYEAEEMERINLEIWRAGKAVSLRPENQK 400
 355 SLEYNQSDPYREKYEAEEMERINLEIWRAGKAVSLRPENQK 396

RESULT 7
 ABJ26502
 ID ABJ26502 standard; protein; 508 AA.

XX AC ABJ26502;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #1160.
 XX KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 XX KW cancer; contamination; biofilm; antibody; immune response.
 XX OS Aspergillus fumigatus.
 XX PN WO200286090-A2.
 XX PD 31-OCT-2002.
 XX PF 23-APR-2002; 2002WO-US013142.
 XX PR 23-APR-2001; 2001US-0285697P.
 XX PR 27-APR-2001; 2001US-0287066P.
 XX PR 05-JUN-2001; 2001US-0295890P.
 XX PR 09-JUL-2001; 2001US-0303899P.
 XX PR 31-AUG-2001; 2001US-0316362P.
 XX PA (ELIT-) ELITRA PHARM INC.
 XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;
 XX DR WPI; 2003-093124/08.
 XX PT New purified or isolated nucleic acids of essential genes of Aspergillus
 XX PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 XX PT or for treating a non-infectious disease in a subject e.g. cancer.
 XX PS Disclosure; Page; 175pp; English.
 XX XX The invention relates to novel purified or isolated nucleic acids of

essential genes of Aspergillus fumigatus. The isolated nucleic acids of
 the invention are used to treat or prevent infections by a pathogenic
 organism such as A. fumigatus, to treat a non-infectious disease in a
 subject (e.g. cancer), to prevent or contain contamination of an object
 by A. fumigatus, or to prevent or inhibit formation on a surface of a
 biofilm comprising A. fumigatus. The polynucleotides are useful for
 expressing recombinant protein for characterisation, screening or
 therapeutic use, as markers for host tissues in which the pathogenic
 organisms invade or reside, for comparing with the DNA sequence of A.
 fumigatus to identify duplicated genes or paralogues having the same or
 similar biochemical activity and/or function, for comparing with DNA
 sequences of other related or distant pathogenic organisms to identify
 potential orthologous essential or virulence genes, for selecting and
 making oligomers for attachment to a nucleic acid array for examination
 of expression patterns, for raising anti-protein antibodies, as an
 antigen to raise anti-DNA antibodies or to elicit another immune
 response, and for identifying polynucleotides encoding the other protein
 with which binding occurs or to identify inhibitors of the binding
 interaction. The polypeptides may be used to raise antibodies or to
 elicit immune response, as a reagent in assays designed to quantitatively
 determine levels of the protein in biological fluids, as a marker for
 host tissues in which pathogenic organism invade or reside, and to
 isolate correlative receptors or ligands in the case of virulence
 factors. This sequence represents a protein of one of the essential genes
 of Aspergillus fumigatus of the invention

Sequence 508 AA;

Query Match 79.7%; Score 1668; DB 6; Length 508;
 Best Local Similarity 79.1%; Pred. No. 1.5e-150;
 Matches 318; Conservative 42; Mismatches 34; Indels 8; Gaps 4;

QY 1 MSARGFSKALRPMARQLATPAVQRSSFVAASMSVRATRKAA--VAPTOOQIRGVKTMDF 58
 113 MASRGLPRALR-LAR-VAAP-----RTVISALPPALAKAATRVAASTAPRGVKTITAF 166

QY 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGKSW 118
 167 DSKETVYERADWPKEKLEFYKDDTLALIGYSGHGGQGLNRLNGLNVIIGVRKDGASW 226

QY 119 KDAVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPAKQITKGTLYFSHGFS 178
 227 KEAQDQWIPGKNLFDLTVAVQKGTIVMNLSDAAQSETWPLKPLITKGTLYFSHGFS 286

QY 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSLFREGRGINSFVAYQDVTGEAEKAI 238
 287 PVFKELTKVDVDPKDVILVAPKSGRTVRSLFREGRGINSFVAYQDVTGEAEKAI 346

QY 239 GVAIGSGVLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 347 GVAIGSGVLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 406

QY 299 EATQSLYPLICANGMDWMYACSTTARRGAIDMSRPFKDALKPVENQLYDSVKGDSGTOR 358
 407 EATQSLYPLICANGMDWMYACSTTARRGAIDMSRPFKDALKPVENQLYDSVKGDSGTOR 466

QY 359 SLDYNQSDPYREKYEAEEMERINLEIWRAGKAVSLRPENQK 400
 467 SLEYNQSDPYREKYEAEEMERINLEIWRAGKAVSLRPENQK 508

RESULT 8
 ABJ25902
 ID ABJ25902 standard; protein; 388 AA.

XX AC ABJ25902;
 XX DT 16-APR-2003 (first entry)
 XX DE Aspergillus fumigatus essential gene protein #560.
 XX KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 XX KW cancer; contamination; biofilm; antibody; immune response.

CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organisms invade or reside, and to
 CC isolate correlative receptors or ligands in the case of virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of *Aspergillus fumigatus* of the invention
 XX
 SQ Sequence 500 AA;

Query Match 78.0%; Score 1634; DB 6; Length 500;
 Best Local Similarity 78.9%; Pred. No. 2.7e-147; Indels 8; Gaps 4;
 Matches 311; Conservative 42; Mismatches 33;
 QY 1 MSARGFSKALRPMARQATPAVQRSSFVAASSMVRATRKAA--VAPTOQQIRGVKTMDF 58
 DB 113 MASRGLPALR-LAR-VAAP----RTVISAALPRPALAKAATRAAATPVRGVKTTAFA 166
 QY 59 GHKEQVWERADWPKEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEK 118
 DB 167 DSKETVYERADWPKEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLE 226
 QY 119 KDAVQDGVNPKNLFVEVDEAISRGTVIMNLLSDAAQSETWPAKPKQITKGTLYFSHGFS 178
 DB 227 KEATQDGVNPKNLFVEVDEAISRGTVIMNLLSDAAQSETWPAKPKQITKGTLYFSHGFS 286
 QY 179 PVFKDLTKVEVPTDVIDCAPKSGRTVRSFLPREGINSFVAVYQDVTGEAEKAI 238
 DB 287 PVFKDLTKVEVPTDVIDCAPKSGRTVRSFLPREGINSFVAVYQDVTGEAEKAI 346
 QY 239 GVAIGSGYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 DB 347 GVAIGSGYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 406
 QY 299 EATQSLYPLIGANGMDWYEAACSTTARRGAIKVPFNQYDVSVDGSETOR 358
 DB 407 EATQSLYPLIGANGMDWYEAACSTTARRGAIKVPFNQYDVSVDGSETOR 466
 QY 359 SLDYNSQPDYREKYEAEMEIRNLEIWRAGKAVRSLRPENQ 399
 DB 467 SLDYNSQPDYREKYEAEMEIRNLEIWRAGKAVRSLRPENQ 400

RESULT 10
 AAU15089
 ID AAU15089 standard; protein; 400 AA.
 XX
 AC AAU15089;
 XX
 DT 04-DEC-2001 (first entry)
 XX
 DE Protein encoded by *C. albicans* essential gene CAVLR355C (ILV5).
 KW Gene identification; essential gene; GRACE; pathogenic fungus;
 KW gene replacement and conditional expression; fungal infection.
 XX
 OS *Candida albicans*.
 XX
 PN WO200160975-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 20-FEB-2001; 2001WO-US005551.
 XX
 PR 18-FEB-2000; 2000US-0183534P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Roemer T, Jiang B, Boone C, Bussey H;
 XX
 DR WPI; 2001-489080/53.
 N-PSDB; AAS23417.

XX Identifying genes essential to fungal metabolisms and identifying
 PT potential therapeutic agents that target these genes.
 XX
 PS Claim 43; Page 222-223; 324pp; English.
 XX
 CC The present invention relates to novel methods for constructing fungal
 CC strains useful for identification and validation of gene products as
 CC targets for therapeutic agents, for creating a collection of identified
 CC essential genes, and screening assays for the discovery of new drugs. The
 CC invention provides the GRACE (gene replacement and conditional
 CC expression) method for the construction of mutant organisms referred to
 CC as GRACE strains of the organism. The invention can be applied to any
 CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,
 CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful
 CC to identify agents that may be used in the treatment of fungal
 CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*
 CC essential genes
 XX
 SQ Sequence 400 AA;

Query Match 72.9%; Score 1526.5; DB 4; Length 400;
 Best Local Similarity 73.8%; Pred. No. 3.9e-137;
 Matches 296; Conservative 49; Mismatches 53; Indels 3; Gaps 3;
 QY 1 MSARGFSKALRPMARQATPAVQRSSFVA--ASSMVRATRKAAVAPTO--QOIRGVKTMDF 58
 DB 1 MSFRITTSRMRVARLATAKATLSKRTFSLANATTRYTAASSAAKAMTPTITSIRGVKTINFG 60
 QY 59 GHKEQVWERADWPKEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEK 118
 DB 61 GTEEVVHERADWPKEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLEKLE 119
 QY 119 KDAVQDGVNPKNLFVEVDEAISRGTVIMNLLSDAAQSETWPAKPKQITKGTLYFSHGFS 178
 DB 120 EAAVQDGVNPKNLFVEVDEAISRGTVIMNLLSDAAQSETWPAKPKQITKGTLYFSHGFS 179
 QY 179 PVFKDLTKVEVPTDVIDCAPKSGRTVRSFLPREGINSFVAVYQDVTGEAEKAI 238
 DB 180 PVFKDLTKVEVPTDVIDCAPKSGRTVRSFLPREGINSFVAVYQDVTGEAEKAI 239
 QY 239 GVAIGSGYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 DB 240 AIAIGSGYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 299
 QY 299 EATQSLYPLIGANGMDWYEAACSTTARRGAIKVPFNQYDVSVDGSETOR 358
 DB 300 EATQSLYPLIGANGMDWYEAACSTTARRGAIKVPFNQYDVSVDGSETOR 359
 QY 359 SLDYNSQPDYREKYEAEMEIRNLEIWRAGKAVRSLRPENQ 399
 DB 360 SLDYNSQPDYREKYEAEMEIRNLEIWRAGKAVRSLRPENQ 400

RESULT 11
 ABP73238
 ID ABP73238 standard; protein; 400 AA.
 XX
 AC ABP73238;
 XX
 DT 30-JAN-2003 (first entry)
 XX
 DE *Candida albicans* essential protein SEQ ID NO 7075.
 KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 KW proliferation; *Candida albicans*; fungicide; antifungal.
 XX
 OS *Candida albicans*.
 XX
 PN WO200253728-A2.
 XX
 PD 11-JUL-2002.

Db 241 GYVQTTTFRVNSDLYGERGCLMGCIHGMFLAQYDVLRENGHSPSEAFNETVEATQSL 300
 QY 305 YPLIGANGMDWYACSTTARRGAIDMSPRFKDALKPVFNOLYDSVKDGSSETQSLSDYNS 364
 Db 301 YPLIGKGYMDWYDACSSTARRGALDWPYIPFNALKPVFQDLYESTKNGTETKSLSENS 360
 QY 365 QPDYREKYEAEMBEIRNLEIWRAGKAVRSIRPENQ 399
 Db 361 QPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 395

RESULT 13
 ADK64188
 ID ADK64188 standard; protein; 395 AA.
 AC
 AC
 AC
 DT 06-MAY-2004 (first entry)
 XX Disease treating protein complex-derived protein #1281.
 DE
 XX protein complex; drug target; diagnosis.
 KW Unidentified.
 OS
 XX
 FN EPI338608-A2.
 XX
 PD 27-AUG-2003.
 XX
 XX 20-DEC-2002; 2002EP-00102902.
 XX
 PR 20-DEC-2001; 2001EP-00130253.
 XX
 XX (CELL-) CELLZOME AG.
 XX
 PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
 PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
 PI Michon A, Leutwein C, Rick J;
 XX
 DR WPI; 2003-638460/61.
 DR N-PSDB; ADK64189.

New proteins and protein complexes from eukaryotes, useful as targets in drug screening, or in diagnosing or screening for the presence of a disease or disorder, or a predisposition for developing a disease or disorder in a subject.

Disclosure; SEQ ID NO 2561; 13pp; English.

The invention relates to novel protein complexes comprising a first and a second protein, or its derivative, fragment, homologue or variant. The proteins are selected from given protein complexes, which are not defined in the specification. The variants are encoded by nucleic acids that hybridize to the nucleic acids encoding the proteins under low stringency conditions. The protein complexes are useful as targets for an active agent of a pharmaceutical. These protein complexes are particularly useful as drugs targets for the treatment or preventing of a disease or disorder. The complexes and methods above are useful in diagnosing or screening for the presence of a disease or disorder or a predisposition for developing a disease or disorder in a subject. These are also useful in screening for a drug for treatment or prevention of a disease or disorder. The molecule that modulates the amount, activity or protein components of the complex is useful for the manufacture of a medicament for the treatment or prevention of a disease or disorder. This sequence corresponds to a protein of the invention. (Note: the sequence data for this patent did not form part of the printed specification but was obtained from the EPO in electronic format).

Sequence 395 AA;

Query Match 71.8%; Score 1503; DB 7; Length 395;
 Best Local Similarity 72.9%; Pred. No. 6.8e-135;

Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;
 QY 10 LRPMARQL--ATPAVORRSFVAASSMVRATRKAA--VAPTQQQIRGVKTMDFAGHKEQV 64
 Db 2 LRTQAARLICNSRVITAKRTFALATRAAAYSRAARFVKP-MITTRGLKQINFGTGVTV 60
 QY 65 WERADWPKEKLLFYKDDTLALIGYSQGHGQGLNLRDNLNVIIGVRKDGKSKWDVOD 124
 Db 61 YERADWPKEKLLDYFKNDTFALIGYSQGHGQGLNLRDNLNVIIGVRKDGASKAAIED 120
 QY 125 GWVPGKNLFEVDRAISRGTVIMNLLSDAAQSETWPAKLPQITKGTLYFSGHGRSPVPKDL 184
 Db 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETWPAKLPQITKGTLYFSGHGRSPVPKDL 180
 QY 185 TKVEVPTDVIDILCAPKSGRTVRSIFREGGINSSPAVYQDVTGEAEKAIAGVAIGS 244
 Db 181 THVEPPKDLVILVAPKSGRTVRSIFPKEGGINSSYAVVNDVTGKAHKAQALAVAIGS 240
 QY 245 GYLYKTTFEKVEYSDLYGERGCLMGCIHGMFLAQYEVLRERHSPSPSEAFNETVEATQSL 304
 Db 241 GYVQTTTFRVNSDLYGERGCLMGCIHGMFLAQYDVLRENGHSPSEAFNETVEATQSL 300
 QY 305 YPLIGANGMDWYACSTTARRGAIDMSPRFKDALKPVFNOLYDSVKDGSSETQSLSDYNS 364
 Db 301 YPLIGKGYMDWYDACSSTARRGALDWPYIPFNALKPVFQDLYESTKNGTETKSLSENS 360
 QY 365 QPDYREKYEAEMBEIRNLEIWRAGKAVRSIRPENQ 399
 Db 361 QPDYREKLEKELDTIRNMEIWKVGEVKRLPENQ 395

RESULT 14
 ADB70124
 ID ADB70124 standard; protein; 409 AA.
 AC
 AC ADB70124;
 XX
 DT 04-DEC-2003 (first entry)
 XX
 DE C. neoformans amino acid sequence SEQ ID NO:3168.
 XX
 KW fungicide; gene therapy; infection.
 XX
 OS Cryptococcus neoformans.
 XX
 XX
 PN WC2003052076-A2.
 XX
 PD 26-JUN-2003.
 XX
 PF 17-DEC-2002; 2002WO-US040225.
 XX
 PR 17-DEC-2001; 2001US-0341261P.
 XX
 PA (ELIT-) ELITRA PHARM INC.
 XX
 PI Zamudio C, Eroshkin AM;
 XX
 XX WPI; 2003-533017/50.
 DR N-PSDB; ADB69041.
 XX
 PT New nucleic acid, useful for preparing a composition for treating an infection caused by Cryptococcus neoformans.
 XX
 PS Claim 9; SEQ ID NO 3168; 136pp; English.

The invention relates to a novel purified or isolated Cryptococcus neoformans nucleic acid molecule comprising a sequence encoding a polypeptide comprising a sequence not given in the specification. A polynucleotide of the invention has fungicide activity, and may have a use in gene therapy. The nucleic acid is useful for preparing a composition for treating an infection caused by Cryptococcus neoformans. The present sequence represents a C. neoformans sequence of the invention. Note: The sequence data for this patent is not represented in

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:27:29 ; Search time 21.1579 Seconds
(without alignments)
1828.118 Million cell updates/sec

Title: US-10-797-248A-1
Perfect score: 2094
Sequence: 1 MSARGFSKALRPMPARQLATP.....EIWRAGKAVRSLRPENQKQK 402

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

1: Pir1.*

2: Pir2.*

3: Pir3.*

4: Pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1856	88.6	400	1 JCI1428	ketol-acid reducto
2	1503	71.8	395	1 A24709	ketol-acid reducto
3	1499.5	71.6	404	2 T40532	ketol-acid reducto
4	490	23.4	342	2 C69644	ketol-acid reducto
5	481.5	23.0	333	2 P70407	acetohydroxy acid
6	479	22.9	331	2 AC1694	ketol-acid reducto
7	475	22.7	331	2 AB1323	ketol-acid reducto
8	473	22.6	332	2 H75044	ketol-acid reducto
9	472	22.5	337	2 A96911	ketol-acid reducto
10	462.5	22.1	336	2 G95051	ketol-acid reducto
11	462.5	22.1	340	2 C84032	ketol-acid reducto
12	462.5	22.1	340	2 C97922	ketol-acid reducto
13	461	22.0	336	2 D72362	ketol-acid reducto
14	455	21.7	348	1 F64492	ketol-acid reducto
15	453.5	21.7	335	2 C90204	ketol-acid reducto
16	449	21.4	367	1 A47037	ketol-acid reducto
17	447	21.3	581	2 T06825	ketol-acid reducto
18	446	21.3	340	2 B86778	ketol-acid reducto
19	441	21.1	591	1 S30145	ketol-acid reducto
20	441	21.1	591	2 T45681	ketol-acid reducto
21	436	20.8	331	2 AD2095	ketol-acid reducto
22	435	20.8	334	2 P89997	ketol-acid reducto
23	428	20.4	344	1 S35440	alpha-keto-beta-hy
24	427	20.4	363	2 C75387	probable ketol-ac
25	427	20.4	595	1 S17180	ketol-acid reducto
26	424	20.2	337	2 F81066	ketol-acid reducto
27	424	20.2	337	2 F81066	ketol-acid reducto
28	409.5	19.6	332	2 H69497	ketol-acid reducto
29	406	19.4	333	2 A69059	ketol-acid reducto

ketol-acid reducto
ketol-acid reducto
acetolactate synth
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto
probable ilvc prot
ketol-acid reducto
ketol-acid reducto
hypothetical prote
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto
ketol-acid reducto

ALIGNMENTS

RESULT 1

JCI1428

ketol-acid reductoisomerase (EC 1.1.1.86) - Neurospora crassa

N/Alternate names: alpha-keto-beta-hydroxylacyl reductoisomerase

C/Species: Neurospora crassa

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 05-Oct-2004

C/Accession: JCI1428

R/Sista: H.; Bowman, B.

Gene 120, 115-118, 1992

A/Title: Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-b-

A/Reference number: JCI1428; MUID:93013010; PMID:1398116

A/Accession: JCI1428

A/Molecule type: DNA

A/Residues: 1-400 <STS>

A/Cross-references: UNIPROT:P38674; UNIPARC:UPI000012D525; GB:M84189; NID:g168821; PTDN:

C/Genetics:

A/Map position: V

A/Introns: 68/1; 78/3; 170/3; 392/3

C/Superfamily: ketol-acid reductoisomerase, fungal type; ketol-acid reductoisomerase hom
C/Keywords: isoleucine-valine biosynthesis; isomerase; mitochondrion; oxidoreductase
F;87-273/Domain: ketol-acid reductoisomerase homology <KAR>

Query Match 88.6%; Score 1856; DB 1; Length 400;
Best Local Similarity 86.8%; Pred. No. 5.2e-134;
Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MSARGFSKALRPMPARQLATPAVQRRSFVAASSMVRAT--RKAAPVPTQQQIRGVKTMDF 58
Db 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAAPARQQVRGVKTMDF 60

Qy 59 GHKEQWERADWPEKLEFVKDDTLALITGYSGHGGQGLNLRDNLNLIIVGRKDKSW 118
Db 61 GHKEVHEHADWPAEKLLDFKNDTLALITGYSGHGGQGLNLRDNLNLIIVGRKDKSW 120

Qy 119 KDAVQDQWPGKMLFEVDEAISRTIVMNLSDAAQSETWPAKLPQITTKGKTLFYSHGFS 178
Db 121 EDALQDQWPGKMLFDVDEAISRTIVMNLSDAAQSETWPHIKPQITTKGKTLFYSHGFS 180

Qy 179 PVFKDLTKVEPTDVIDVILCAPKSGRTVRSLPREGGINSSPAVYQDVTGEAEKAI 238
Db 181 PVFKDLTKVEPTDVIDVILVAPKSGRTVRSLPREGGINSSPAVYQDVTGKAKEAVAL 240

Qy 239 GVAIGSGYLKTTTFEKEVYSDLYGERGCLMGHGHFLAQYEVLRERGHSPSEAFN 298
Db 241 GVAIGSGYLKTTTFEKEVYSDLYGERGCLMGHGHFLAQYEVLRERGHSPSEAFN 300

Qy 299 EATQSLYPLIGANGMDWMYACSTTARRGAIDWSRPFKDALKPFVNOLYDVSVDGSG 358
Db 301 EATQSLYPLIGANGMDWMDFACSTTARRGAIDWTPFKDALKPFVNOLYDVSVDG 360

Qy 359 SLDYNQPDYREKYEAEMEIRNLEIWRAGKAVRSLRPENQK 400

keto-acid reductoisomerase ilvC - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 05-Oct-2004
C:Accession: C69644
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Ch
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gall
lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsteppel, S.; Hosono, S.; Hulio, M.F.
Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maue
Y. M.; Ogawa, K.; Ogiwara, K.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetel
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadie, Y.; Sato, T.; Scanlon
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, P.; Segikuchi, J.; Sekowska, A.; Seron
akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama
T.; Winters, P.; Wipat, A.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, M.
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: C69644
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-342 <KUN>
A:Cross-references: UNIPROT:P37253; UNIPARC:UPI00000380DE; GB:Z99118; GB:AL009126; NID:9
A:Experimental source: strain 168
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductois
F:21-202/Domain: keto-acid reductoisomerase homology <KAR>
Query Match 23.4%; Score 490; DB 2; Length 342;
Best Local Similarity 36.7%; Pred. No. 8.6e-30;
Matches 122; Conservative 68; Mismatches 118; Indels 24; Gaps 11;
Qy 72 KEKLEVPKDDTLALIGVSGHGGQGLNRLDGLNVLIVGRKDGKSKWDAVDQGWVPGKN 131
Db 11 KENVL---AKTVAVIGVSGHGHALNKLKESGVDDVIVGVGRQ-GKSFQAGD---GHK 62
Qy 132 LFEVDEAISRGTVIMNLLSDAAQSETWPA-LKPQITKGKTLFVSHGSPFVKDLTKVEVP 190
Db 63 VFSVKEAAQAQAEIIMVLLPDEQQKVEAEIKBELTAGKSLVFAHGFNVHFHIVP---P 119
Qy 191 TDVDVILCAPKSGRTVRSFLPREGRGINSFVQDVVTGAEKALGVAIG---SGYL 247
Db 120 ADVDDVFLVAPKPGHLVRRTYEQAGVPALFAIQDVTGEARDKALAYAKIGGARAGVL 179
Qy 248 YKTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNFTVEATQSLYPL 307
Db 180 -ETTFKEETDLDLFGQVLCGLSLVAKAGFETLTAGYQPELAVFECLHE-LKLVLDL 237
Qy 308 IGANGMDMYEACSTTARRGAIDMSPRFKDA-LKPFVNLQYDSVDGSETQRSIDYN--S 364
Db 238 MYEGLAGMYSISDTAQWGDVFSVPRVDDKVKESKMKVLDIQNGTFAKENVIVENQVN 297
Qy 365 QPDYREKYEAEIRNLEIWRAGKAVRSRNP 396
Db 298 RPRFNAINASENEH---QIEVVGRKLRNMP 325
RESULT 5
F70407
acetohydroxy acid isomerase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 05-Oct-2004
C:Accession: F70407
R:Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98156666; PMID:9537320
A:Accession: F70407
A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-333 <AQF>
A:Cross-references: UNIPROT:O67289; UNIPARC:UPI0000056582; GB:AB000730; NID:G2983674; P1
A:Experimental source: strain VF5
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductois
F:21-203/Domain: keto-acid reductoisomerase homology <KAR>
Query Match 23.0%; Score 481.5; DB 2; Length 333;
Best Local Similarity 33.3%; Pred. No. 3.7e-29;
Matches 110; Conservative 72; Mismatches 135; Indels 13; Gaps 6;
Qy 70 WPKEKLEVPKDDTLALIGVSGHGGQGLNRLDGLNVLIVGRKDGKSKWDAVDQGWVPG 129
Db 6 YDEASIDILKDVIAILGVSGHGHALNRLDGLNVLIVGRKDGKSKWDAVDQGWVPG 62
Qy 130 KNLFEVDEAISRGTVIMNLLSDAAQSETWTP-ALKPQITKGKTLFVSHGSPFVKDLTKVE 188
Db 63 -EYVTPREAAKRAADIIMFLPDTVQPEVYKNEVEPELNSKTLTFAFHGFNIHFQIVP-- 119
Qy 189 VPTDNDVILCAPKSGRTVRSFLPREGRGINSFVQDVVTGAEKALGVAIGS--GY 246
Db 120 -PKDNDVFWVAPKPGHLVRRMYTEKGVPALVAHQDASGTCCKALAYAKIGATRAG 178
Qy 247 LYKTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFNFTVEATQSLYPL 306
Db 179 VIETTFKEETDLDLFGQVLCGLVTLIKAGFETLVNAGYQPEVAVFECLHE-LKLVLD 237
Qy 307 LIGANGMDMYEACSTTARRGAIDMSPRFKDAKLPFNQYDSVDGSETQRSIDYNSQP 366
Db 238 LIYEHGIGMYSISDTAKYGVDTGRGRIYKVKVPYMEKTLLEIQGFEAREWILENKAG 297
Qy 367 DYREKYEAEIRNLEIWRAGKAVRSRNP 396
Db 298 --RPVYVALLERDRHLVREKVGSELKRMPP 325
RESULT 6
AC1694
keto-acid reductoisomerase (acetohydroxy-acid isomerase) homolog ilvC [imported]
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004
C:Accession: AC1694
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Psihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Psihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, P.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauget, O.; Entian, K.D.; Psihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: AC1694
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-331 <GLA>
A:Cross-references: UNIPARC:UPI00000CC759; GB:AL592022; PIDN:CAC97323.1; PID:gl6414607;
A:Experimental source: strain Clp11262
C:Genetics:
A:Gene: ilvC
C:Superfamily: keto-acid reductoisomerase, archaea/bacteria type, keto-acid reductoisom
Query Match 22.9%; Score 479; DB 2; Length 331;
Best Local Similarity 36.1%; Pred. No. 5.7e-29;
Matches 120; Conservative 59; Mismatches 129; Indels 24; Gaps 10;
Qy 78 YPKD-----DTLALIGVSGHGGQGLNRLDGLNVLIVGRKDGKSKWDAVDQGWVPG 128
Db 5 YVEDAVKNALBEGKTAVVIGVSGHGHALNRLDGLNVLIVGRKDGKSKWDAVDQGWVPG 61
Qy 129 GKNLFEVDEAISRGTVIMNLLSDAAQSETWTP-ALKPQITKGKTLFVSHGSPFVKDLTKV 187
Db 62 --DVYSVSEAEKADVIMILLPDTQGETYENEIKNKGALNVLFAHGFNIHF---DVI 116

QY	188	EVPTDQVILCAPKSGRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIGS--G	245
Db	117	NPSPDQVFLVAPKPGHLVRRTFVEGGAVPSLFAIQDQATGNARTALSAYAKIGATRA	176
QY	246	YLKTTTFEKEVSDLYGERGCLMGHMFQAQYEVLRERGHSPSAFNETVEEATQSLY	305
Db	177	GVITETTFKEETEDLFGQAVLCGGATHLIQAGFETLVEAGYQPELAYPEVLHE-MKLIV	235
QY	306	PLIGANGDMWYACSTTARRGAIDWSPRFKDA-LKPVFNQLYDSVKDQSETQSRSLDYN	364
Db	236	DLMYEGMEKORHSISNTAIEGYDVGSPRVVTADTKKAMKEVLTDIQNGNFAKSFINDNK	295
QY	365	QPDYREKYAEEMEIRNLNLEIWRAGKAVRSILRP	396
Db	296	N-GFKEFHRMKEQ-QGHQIEKVGAEIREMMP	325
RESULT 7			
AB1323			
ketol-acid reductoisomerase (acetohydroxy-acid isomeroreductase) homolog ilvC [imported]			
C:Species: Listeria monocytogenes			
C>Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 05-Oct-2004			
C:Accession: AB1323			
R:Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.; D.; Jones, L.M.; Karst, U.			
Science 294, 849-852, 2001			
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland, A.; Title: Comparative genomics of Listeria species.			
A:Reference number: AB1077; MUID:21537279; PMID:11679669			
A:Accession: AB1323			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-331 <KLA>			
A:Cross-references: UNIPARC:UPI0000054FP8; GB:NC_003210; PIDN:CAD00064.1; PID:gi6411439;			
A:Experimental source: strain EGD-e			
C:Genetics:			
A:Gene: ilvC			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase			
Query Match 22.7%; Score 475; DB 2; Length 331;			
Best Local Similarity 35.8%; Pred. No. 1.1e-28;			
Matches 119; Conservative 61; Mismatches 128; Indels 24; Gaps 10;			
QY	78	YFKD-----DTLALICYGQGHGQGLNLRDNGLVIIQVRKDGKSWKDAVQDGWVP	128
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QY	129	GKNLFEVDEAISRGTVIMNLLSDAAQSETWP-ALKPQITKGTLYFSHGSPVPKDLTKV	187
Db	62	--DVIVSSEADKADVIMILLPDETQGETYENIKNLKAGNSLVFAHGFNIHF---DVI	116
QY	188	EVPTDQVILCAPKSGRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIGS--G	245
Db	117	NPSPDQVFLVAPKPGHLVRRTFVEGGAVPSLFAIQDQATGNARTALSAYAKIGATRA	176
QY	246	YLKTTTFEKEVSDLYGERGCLMGHMFQAQYEVLRERGHSPSAFNETVEEATQSLY	305
Db	177	GVITETTFKEETEDLFGQAVLCGGATHLIQAGFETLVEAGYQPELAYPEVLHE-MKLIV	235
QY	306	PLIGANGDMWYACSTTARRGAIDWSPRFKDA-LKPVFNQLYDSVKDQSETQSRSLDYN	364
Db	236	DLMYEGMEKORHSISNTAIEGYDVGSPRVVTADTKKAMKEVLTDIQNGNFAKSFINDNK	295
QY	365	QPDYREKYAEEMEIRNLNLEIWRAGKAVRSILRP	396
Db	296	N-GFKEFHRMKEQ-QGHQIEKVGAEIREMMP	325
RESULT 8			
H75044			
ketol-acid reductoisomerase (ilvC) PAB0889 - Pyrococcus abyssi (strain Orsay)			
C:Species: Pyrococcus abyssi			
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 05-Oct-2004			
C:Accession: H75044			
R:anonymous, Genoscope			
submitted to the EMBL Data Library, July 1999			
A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru			
A:Reference number: A75001			
A:Accession: H75044			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-332 <KAW>			
A:Cross-references: UNIPROT:O9UZ09; UNIPARC:UPI000003453B; GB:AJ248287; GB:AL096836; NID:			
A:Experimental source: strain Orsay			
C:Genetics:			
A:Gene: ilvC; PAB0889			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase			
F;24-206/Domain: ketol-acid reductoisomerase homology <KAR>			
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Best Local Similarity 35.4%; Pred. No. 1.6e-28;			
Matches 116; Conservative 71; Mismatches 123; Indels 18; Gaps 9;			
QY	73	EKLRYFFKDDTLALICYGQGHGQGLNLRDNGLVIIQVRKDGKSWKDAVQDGWVPKQL	132
Db	12	EVSMDILKDKTVAVIGYGNQGEAQAKNRDSCGVHVLGLRPSGSSWKRAEKDGF---EV	67
QY	133	FEVDEAISRGTVIMNLLSDAAQSETWP-PALKPQITKGTLYFSHGSPVPKDLTKVEVPT	191
Db	68	YTIEAVKRAIDVHILIPDLVQPKVYREHIEPYLRGQALGFSGHGFNIHYKQIVP---PE	124
QY	192	DVDVILCAPKSGRTVRSILFREGRGINSFVAVYQDVVTGEABEKAIALGVAIG---SGYLY	248
Db	125	YDVIMVAPKSPGKRVREKYLEGFGVPALVAVIYQDVTGNAKOLALAWAKAIGCTRAGVI-	183
QY	249	KTTTFEKEVSDLYGERGCLMGHMFQAQYEVLRERGHSPSEAFNETVEEATQSLYPLI	308
Db	184	ETTFKDESDLIGQLVLGGLIELIKKGFVELGYPPPELAYFEACNEA-KLIMDLI	242
QY	309	GANGDMWYACSTTARRGAIDWSPR-FKDALKVPFNQLYDSVKDQSETQSRSLDYNQDP	367
Db	243	YERGTGMLKAVSDTAKYGLTVGPKVIDDDHVKNMKKFAERVRSQ---EFAKEWISKAD	299
QY	368	-VREKYAEEMEIRNLNLEIWRAGKAVRSL	394
Db	300	KASEVLEELMKFIEHEIEKVGKRFIRKM	327
RESULT 9			
A96911			
ketol-acid reductoisomerase [imported] - Clostridium acetobutylicum			
C:Species: Clostridium acetobutylicum			
C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 05-Oct-2004			
C:Accession: A96911			
R:Nolling, J.; Breton, G.; Onelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.			
J. Bacteriol. 193, 4823-4838, 2001			
A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Clo			
A:Reference number: A96900; MUID:21359325; PMID:21359325			
A:Accession: A96911			
A>Status: preliminary			
A:Molecule type: DNA			
A:Residues: 1-337 <KUR>			
A:Cross-references: UNIPROT:Q97MV0; UNIPARC:UPI00000C9D5C; GB:AE001437; PIDN:AAK78076.1;			
A:Experimental source: Clostridium acetobutylicum ATCC824			
C:Genetics:			
A:Gene: CAC0091			
C:Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisomerase			
Query Match 22.5%; Score 472; DB 2; Length 337;			
Best Local Similarity 34.2%; Pred. No. 2e-28;			
Matches 115; Conservative 65; Mismatches 132; Indels 24; Gaps 9;			

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Qy 76 LEYKDDTLALIGYSGHGGIINLRDNLNLIIVGVRKDGSKWDKAVODGWVPGKNLFEV 135
Db 14 LNYLKKKIALIGSGGHAHALKESGLNVLVGLYDGSKSWKVAEDYGF-----EYVEF 69

Qy 136 DEAIISRGTVINMLISDAASQETWPA-LKPQITKGTLYFSGHGFSPVKDLTKVEVPTDVD 194
Db 70 ADAYKQAVQVWMLLPDEKQKIYEASIKONLDEGDAFFAAGFNHYNQIVP-----PKNVD 126

Qy 195 VILCAPKSGRTVSLFRGGRGINSFVAVQDVTGEABEAKAIALGVAIG--SGYLYKTTTF 252
Db 127 VLMIAPIKPGHIVRRQYTGEGGVCLYAVHODYTGKGEIKALAYGKGIGGKGGWMTTF 186

Qy 253 EKEVYSDLYGRCGLMGHGMFLAQYEVLRERHSPSEAFNEVEATQSLYPLIGANG 312
Db 187 KIETETDLFGQAVLCGICALINAGYDTLREAGYSAENAYFECHF--MKMIVDLMYEGG 245

Qy 313 MDMMYEACSTTARRGAIDWSR-PKDALKPVFNLVDSVKDGSQTSRSL--DYNQSDYR 369
Db 246 MAKWYSISDTAEYGVVGNRLINDNVRAEMKKVLTETIQDGTFAKWILLENQTRGPAFN 305

Qy 370 EKYAEEMEEIRNLEIWRAKAVRSL-----RPNQ 399
Db 306 ARRIEADR----EIEVKGRKLRGMGWINENPNS 337

RESULT 10
G95051
ketol-acid reductoisomerase [imported] - Streptococcus pneumoniae (strain TIGR4)
C:Species: Streptococcus pneumoniae
C>Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 05-Oct-2004
C:Accession: G95051
R:Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid-
nson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel,
nson, T.; Hickey, E.K.; Holt, I.E.
Science 293, 498-506, 2001
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison,
A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUID:21357209; PMID:11463916
A;Accession: G95051
A;Molecule type: DNA
A;Residues: 1-336 <KUR>
A;Cross-references: UNIPROT:Q97SD7; UNIPARC:UPT000000C9C91; GB:AE005672; PIDN:AAK74608.1;
A;Experimental source: strain TIGR4
C:Genetics:
A;Gene: SP0447
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom-
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Query Match 22.1%; Score 462.5; DB 2; Length 336;
Best Local Similarity 36.3%; Pred. No. 1.1e-27;
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Qy 76 LEYKDDTLALIGYSGHGGIINLRDNLNLIIVGVRKDGSKWDKAVODGWV 127
Db 1 MEYKDVKVAALDGKKTAVIGYSGGHAHAQNLRDSDGVIIIGVR-PGKSFDRKAKEDGF- 58

Qy 128 PGKNLFEVDAISRGTVINMLISDAASQETWPA-LKPQITKGTLYFSGHGFSPVKDLTK 186
Db 59 ---DVTVAEATKLADVIMILADEIQEILYEAIAPNEAGNAVGFANGFNTHFE---F 112

Qy 187 VEYPTDVLDPKAPKSGRTVSLFRGGRGINSFVAVQDVTGEABEAKI--ALGVAIGS 244
Db 113 IKVPADVDDVPMCAKPGHGLVRRTYERGFVGPVAVYQDQATGNNAKNIAMDCKVGCAAR 172

Qy 245 GYLYKTTTFEYVSDLYGRCGLMGHGMFLAQYEVLRERHSPSEAFNEVEATQSL 304
Db 173 VGLLETTYKRETEEDLFGQAVLCGGTLALIRAGFEVLTEAGYAPELAYFEVLHE--MKLI 231

Qy 305 YPLIGANGMDMYEACSTTARRGAIDWSR-PKDALKPVFNLVDSVKDGSQTSRSLDYN 363
Db 232 VDLIYEGGPKMKQISNTAEYGDYVSGPRVITEQVKENMKAVLADIQNGKPFANDFW-- 289

Qy 364 SQPDY---REKYAEEMEEIRNLEIWRAKAVRSLRP 396
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Db 290 ---DYKAGRPKLTAAYREQAANLEIKVGABLRKAMP 322
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RESULT 11

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C84032
ketol-acid reductoisomerase ilvC [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C>Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 05-Oct-2004
C:Accession: C84032
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.; Hira-
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C84032
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <STO>
A;Cross-references: UNIPROT:Q9K8E7; UNIPARC:UPT000012D53B; GB:AF001517; GB:BA000004; NID
A;Experimental source: strain C-125
C:Genetics:
A;Gene: ilvC
C;Superfamily: ketol-acid reductoisomerase, archaea/bacteria type; ketol-acid reductoisom-
er
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Query Match 22.1%; Score 462.5; DB 2; Length 340;
Best Local Similarity 35.4%; Pred. No. 1.1e-27;
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Db 19 TVAILIGYSGGHAHAQNLRDSDGVIIIGVR-PGKSWDKAAEDGF---QYYSVREAAASRA 73

Qy 143 TVIMNLLSDAAQSETWPA-LKPQITKGTLYFSGHGFSPVKDLTKVEVPTDVIDVILCAPK 201
Db 74 DVIMILLPDEHQPTVYKNEIEPSELSEKTLAFAGFNHYNQIVP---PATVDVFLAAPK 130

Qy 202 GSGRTVSLFRGGRGINSFVAVQDVTGEABEAKAIALGVAIGSY--LYKTTFEKEVYSD 259
Db 131 GPCHLVRRTYVDCGAVGVLVAVYQDQATGQAKIALAYSKMNGSARAGVITTTQEETETD 190

Qy 260 LYGERCLMGHGMFLAQYEVLRERHSPSEAFNEVEATQSLYPLIGANGMDMYEAC 319
Db 191 LFGEQAVLCGGTSALVKGAFETLVEAGYQPEVAYFECLHE-LKLIIVDLMYEGGLEYNRY 249

Qy 320 CSTTARRGAIDWSRPFKDA-LKEVFNQLYDSVKDGS-----ETQKSLDYNQSDPYREK 371
Db 250 ISDTAQGDFQAGPRVVTATKQAKMDILSDIQTGKFAKWILENQAN-----RPE 300

Qy 372 YEAEEMEEIRNLEIWRAKAVRSLRP 396
Db 301 FTAINEREKNHPLLEVVGRELREMP 325
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RESULT 12

C97922

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C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 05-Oct-2004
C:Accession: C97922
R:Hoskins, J.A.; Alborn Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; DeHoff, B.S.; E-
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M-
Y, P.; Sun, P.M.; Winkler, M.E.
J. Bacteriol. 183, 5709-5717, 2001
A:Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaskunas, S.R.;
A;Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
A;Reference number: A97872; MUID:21429245; PMID:11544234
A;Accession: C97922
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-340 <KUR>
A;Cross-references: UNIPROT:Q8DR03; UNIPARC:UPT000005143B; GB:AE007317; PIDN:AAK99207.1;
C:Genetics:
A;Gene: ilvC
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Job time : 22.1579 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 125.94 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248A-1

Perfect score: 2094

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	2081	99.4	400	Q52F28_MAGGR	Q52f28 magnaportha
2	1881	89.8	402	ILV5_NEUCR	P38674 neurospora
3	1861.5	88.9	400	Q4HY40_GIBZE	Q4hy40 gibberella
4	1675	80.0	508	Q4WY40_ASPFU	Q4wy40 aspergillus
5	1673	79.9	400	Q5BA44_EMENI	Q5ba44 aspergillus
6	1581.5	75.5	398	Q5CAP8_YARLI	Q5caf8 yarrowia li
7	1542	73.6	399	Q6BL24_DEBHA	Q6bl24 debaryomyce
8	1530	73.1	397	Q6CY71_KIULA	Q6cy71 kluyveromyce
9	1526.5	72.9	400	Q59W55_CANAL	Q59w55 candida alb
10	1524.5	72.8	400	Q59X88_CANAL	Q59x88 candida alb
11	1505.5	71.9	399	Q6FXG6_CANGA	Q6fxg6 candida gla
12	1503	71.8	395	ILV5_YEAST	P06168 saccharomyc
13	1501	71.7	395	Q02341_YEAST	Q02341 saccharomyc
14	1499.5	71.6	404	ILV5_SCHPO	P78827 schizosacch
15	1489	71.1	395	Q02340_YEAST	Q02340 saccharomyc
16	1467.5	70.1	394	Q075C4_ASHGO	Q075c4 ashbya gos
17	1433.5	68.5	401	Q550A8_CRYNE	Q55q48 cryptococcu
18	1433.5	68.5	401	Q550A8_CRYNE	Q55q48 cryptococcu
19	1416.5	67.6	401	Q96V25_CRYNE	Q96v25 cryptococcu
20	1253	59.8	625	Q4P572_USITWA	Q4p572 ustilago ma
21	1119	53.4	352	Q04135_9FUNG	Q04135 piromyces s
22	1102.5	52.7	362	Q5L9U3_BACFN	Q5l9u3 bacteroides
23	1102.5	52.6	359	Q0A612_BACFN	Q0a612 bacteroides
24	1100.5	52.6	347	Q64P11_BACFR	Q64p11 bacteroides
25	1043	49.8	344	Q847R5_ASTYP	Q847r5 aster yello
26	510.5	24.4	341	Q5KWJ2_GEOKA	Q5kwj2 geobacillus
27	507	24.2	342	Q8RL86_BACST	Q8rl86 bacillus st
28	494	23.6	331	ILV5_PVRFU	Q8u2a3 pyrococcus
29	490	23.4	342	ILV5_BACSU	P37233 bacillus su
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31	479	22.9	331	ILV5_LISIN	Q92a29 listeria in

RESULT 1

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DE	Hypothetical protein.				
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OS	Magnaportha grisea 70-15.				
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;				
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OX	NCBI_TaxID=242507;				
RN	[1]				
RP	NUCLEOTIDE SEQUENCE.				
RC	STRAIN=70-15;				
RA	Biren B., Nusbaum C., Abebe A., Abouelleil A., Adekoya E.,				
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RA	Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,				
RA	Bayul T., Blitshsteyn B., Bloom T., Blye J., Boguslavsky L.,				
RA	Borowsky M., Boukgalter B., Brunache A., Butler J., Calixte N.,				
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RA	Collamore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,				
RA	David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,				
RA	Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,				
RA	Ericksen J., Farina L., Fero S., Ferreira P., Fischer H.,				
RA	Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,				
RA	Gairke A., Goyette A., Graham J., Grandbois E., Gyaltzen K., Hafez N.,				
RA	Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,				
RA	Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,				
RA	Jaffe D., Jones C., Kamal M., Kamat A., Kamvyselis M., Karlsson E.,				
RA	Kells C., Kieu A., Kiser P., Kodira C., Kulbokas E., Labutti K.,				
RA	Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,				
RA	Lindblad-toh K., Liu X., Lokyitsang T., Lokyitsang Y., Lucien O.,				
RA	Lui A., Ma L.J., Mabbitt R., Macdonald J., Maclean C., Major J.,				
RA	Manning J., Marabella R., Maru K., Matthews C., Mauceli E.,				
RA	McCarthy M., McDonough S., McGhee T., Meldrim J., Meneus L.,				
RA	Mesirov J., Mihalav A., Mihova T., Mikkelson T., Mlenga V., Moru K.,				
RA	Mozes J., Mulrain I., Munson G., Naylor J., Neues C., Nguyen C.,				
RA	Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,				
RA	Norbu N., O'donnell P., O'leary S., O'motoh B.,				
RA	O'Neill K., Osman S., Parker S., Perrin D., Phunkthong P., Pignani B.,				
RA	Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,				
RA	Retta R., Richardson S., Rise C., Rodriguez J., Rogers J., Rogov P.,				
RA	Rutman M., Schupbach R., Seaman C., Settupalli S., Sharpe T.,				
RA	Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,				
RA	Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,				
RA	Stetson K., Stone C., Stone S., Stubbs M., Talamas J., Tchuinga P.,				
RA	Tenzing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,				
RA	Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,				
RA	Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,				
RA	Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,				
RA	Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,				
RA	Zimmer A., Zody M., Lander E.;				

32	479	22.9	331	1	ILV5_LISNF	Q7ly36 listeria mo
33	476.5	22.8	336	2	ILV5_BACCL	Q73ba1 bacillus ce
34	476.5	22.8	336	2	Q6HLF4_BACHK	Q6hlf4 bacillus th
35	476.5	22.8	336	2	Q63DX9_BACCC	Q63dx9 bacillus ce
36	475	22.7	328	1	ILV5_PYRAE	Q8ztel pyrobaculum
37	475	22.7	331	1	ILV5_LISMO	Q8y580 listeria mo
38	473.5	22.6	338	1	ILV5_BACCR	Q8y580 listeria mo
39	473	22.6	332	1	ILV5_PYRAB	Q8y580 listeria mo
40	472	22.5	337	1	ILV5_CLOAB	Q9uz09 pyrococcus
41	472	22.5	341	2	Q5WEN2_BACSK	Q97mw0 clostridium
42	472	22.5	342	2	Q65GI7_BACID	Q5wen2 bacillus cl
43	469.5	22.4	336	1	ILV5_BACAN	Q65gi7 bacillus li
44	464.5	22.2	340	2	Q5LXV0_STR11	Q8lt69 bacillus an
45	464.5	22.2	340	2	Q5M2F2_STR12	Q5lxx0 streptococc
						Q5m2f2 streptococc

ALIGNMENTS

```

RT  "The genome sequence of Magnaporthe grisea.";
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN  [2]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=70-15;
RA  Dean R., Mitchell T., Brown D., Pan H., Thon M.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
RN  [3]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=70-15;
RA  Zhu H., Blackmon B.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- CAUTION: The sequence shown here is derived from an
CC  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC  preliminary data.
DR  EMBL: AACU01000121; EAA56157.1; -; Genomic_DNA.
DR  InterPro; IPR000506; ACh_isomrdctse.
DR  Pfam; PF01450; ILVC; 1.
DR  TIGRFAMs; TIGR00465; ilvc; 1.
KW  Hypothetical protein.
SQ  SEQUENCE 400 AA; 44723 MW; 4C89B9E1495B6D75 CRC64;

Query Match          99.4%; Score 2081; DB 2; Length 400;
Best Local Similarity 99.8%; Pred. No. 6e-141;
Matches 399; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY  1  MSARGFSKALRPWARQLATPAVORRSPFAASSWVRATRKAAVAPTQOQIRGVKTMDFAGH 60
DB  1  MSARGFSKALRPWARQLATPAVORRSPFAASSWVRATRKAAVAPTQOQIRGVKTMDFAGH 60

QY  61  KEQWERADWPKEKLLFEYFKDDTLALITYGSGHQGLNLRDNLNLIIVGRKDGKSWKD 120
DB  61  KEQWERADWPKEKLLFEYFKDDTLALITYGSGHQGLNLRDNLNLIIVGRKDGKSWKD 120

QY  121  AVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSTWPAKLPQITKGTLYPSHGFSVP 180
DB  121  AVQDGWVPGKNLFEVDRAISRGTVIMNLLSDAAQSTWPAKLPQITKGTLYPSHGFSVP 180

QY  181  FKDLTKVEVPTDNDVILCAPKSGRTVRSIFRGRGINSSFAVYQDVGTGAEEKALALGV 240
DB  181  FKDLTKVEVPTDNDVILCAPKSGRTVRSIFRGRGINSSFAVYQDVGTGAEEKALALGV 240

QY  241  AIGSGYLYKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNEITVEEA 300
DB  241  AIGSGYLYKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNEITVEEA 300

QY  301  TQSLYPLIGANGDMWYEAQSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDQSETQSRSL 360
DB  301  TQSLYPLIGANGDMWYEAQSTTARRGAIDWSPRFKDALKPFVNQLYDSVKDQSETQSRSL 360

QY  361  DYNQSDPYREKYAEEMEIEINLEIWRAGKAVRSI.RPENQK 400
DB  361  DYNQSDPYREKYAEEMEIEINLEIWRAGKAVRSI.RPENQK 400

RESULT 2
ILV5_NEUCR
ID  ILV5_NEUCR STANDARD; PRT; 402 AA.
AC  P38674; Q7RVDS5; Q8X019;
DT  01-FEB-1995 (Rel. 31, Created)
DT  10-OCT-2003 (Rel. 42, Last sequence update)
DT  13-SEP-2005 (Rel. 48, Last annotation update)
DE  Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE  (Acetylhydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacyl
DE  reductoisomerase).
GN  Names=ilv-2; ORFNames=B11H24.150, NCU03608;
OS  Neurospora crassa.
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC  Sordariomycetidae; Sordariales; Sordariales; Neurospora.
OX  NCBI_TaxID=5141;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.

RX  MEDLINE=93013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;
RA  Sista H., Bowman B.;
RT  "Characterization of the ilv-2 gene from Neurospora crassa encoding
RT  alpha-keto-beta-hydroxyacyl reductoisomerase.";
RL  Gene 120:115-118(1992).
RN  [2]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=74-OR23-1A / FGSC 987;
RX  MEDLINE=22542210; PubMed=12655011; DOI=10.1038/nar/gk9293;
RA  Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Aign V.,
RA  Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
RA  Schulte U.;
RT  "What's in the genome of a filamentous fungus? Analysis of the
RT  Neurospora genome sequence.";
RL  Nucleic Acids Res. 31:1944-1954(2003).
RN  [3]
RP  NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC  STRAIN=74-OR23-1A / FGSC 987;
RX  MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA  Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
RA  Jaffe D., FitzHugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B.,
RA  Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA  Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A.,
RA  Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L.,
RA  Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C.,
RA  Marcotte E., Greenberg D., Roy A., Foley K., Naylor J.,
RA  Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kamvysellis M.,
RA  Mauceli E., Bielke C., Rudd S., Frisman D., Krystofova S.,
RA  Rasmussen C., Metzenberg R.L., Perkins D.D., Kroken S., Cogoni C.,
RA  Macino G., Catchside D.F.A., Li W., Pratt R.J., Osmari S.A.,
RA  DeSouza C.P.C., Glass N.L., Orbach M.J., Berglund J.A., Voelker R.,
RA  Varden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R.,
RA  Natvig D.O., Alex L.A., Mannhaupt G., Ebbola D.J., Freitag M.,
RA  Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.W.;
RT  "The genome sequence of the filamentous fungus Neurospora crassa.";
RL  Nature 422:859-868(2003).
CC  -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+)
CC  = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
CC  -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate +
CC  NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
CC  -1- COFACTOR: Magnesium.
CC  -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
CC  isoleucine from 2-oxobutanoate: step 2.
CC  -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
CC  from pyruvate: step 2.
CC  -1- SUBCELLULAR LOCATION: Mitochondrial.
CC  -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.

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removed.
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EMBL: M84189; AAB00797.1; -; Genomic DNA.
EMBL: AL670005; CAD21284.1; -; Genomic DNA.
EMBL: AABX01000270; EAA32099.1; -; Genomic DNA.
PIR: JCI428; JCI428.
HSSP: Q9HVA2; LNP3.
DR  InterPro; IPR000506; ACh_isomrdctse.
DR  Pfam; PF01450; ILVC; 1.
DR  TIGRFAMs; TIGR00465; ilvc; 1.
KW  Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
KW  Magnesium; Mitochondrion; NADP; Oxidoreductase; Transist peptide.
FT  TRANSIT 1 26 Mitochondrion (Potential).
FT  CHAIN 27 402 Ketol-acid reductoisomerase.
FT  NE BIND 90 99 NADP (Potential).
FT  ACT SITE 177 177 Potential.
FT  ACT SITE 358 358 T -> R (in Ref. 1).
FT  CONFLICT 392 393 Missing (in Ref. 1).
FT  CONFLICT 392 393 Missing (in Ref. 1).
SQ  SEQUENCE 402 AA; 44623 MW; 246F795898D2A174 CRC64;

Query Match          89.8%; Score 1881; DB 1; Length 402;

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[illegible]

QY	296	TVEEATQSLYPLIGANGDMWYEAACSTTARRGALDWSRPFKDALKPVFNOLYDSVKDC	
Db	301	TVEEATQSLYPLIGANGDMWYEAACSTTARRGALDWSRPFKDALKPVFNLSYDAVKDC	
QY	356	TORSLDYNSQDPYRKYEAEHMEIRNLEIWRAGKAVRSLRPENOK 400	
Db	361	TKRSLEYNQDPYRKYEAEHMEIRNLEIWRAGKAVRSLRPENOK 405	
RESULT 4			
Q4WYW4	ASPFU		
ID	Q4WYW4	PRELIMINARY;	PRT; 508 AA.
AC	Q4WYW4	ASPFU	
DT	13-SEP-2005	(TREMBLrel. 31, Created)	
DT	13-SEP-2005	(TREMBLrel. 31, Last sequence update)	
DT	13-SEP-2005	(TREMBLrel. 31, Last annotation update)	
DE	DE	Ketol-acid reductoisomerase.	
GN	ORFName=AFuGj4490;		
OS	Aspergillus fumigatus AF293.		
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;		
OC	Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus;		
NCBI	TaxID=330879;		
RP	[1]_TaxID=330879;		
RP	NUCLEOTIDE SEQUENCE.		
RC	STRAIN=AF293;		
RA	Nierman W., Pain A., Anderson M.J., Wortman J., Kim H.Stanley.,		
RA	Arroyo J., Berrihan M., Abe K., Archer D.B., Bermejo C., Bennett J.,		
RA	Bowyer P., Chen D., Collins M., Coulsen R., Davies R., Dyer P.S.,		
RA	Farman M., Fedorova N., Fedorova N., Feldblyum T., Kulkarni R.,		
RA	Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,		
RA	Goldman G.H., Gomi K., Griffith-Jones S., Gwilliam R., Haas B.,		
RA	Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,		
RA	Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,		
RA	Kumagai T., Lafton A., Latge J.-P., Li W., Lord A., Lu C.,		
RA	Majors W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod		
RA	Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,		
RA	Penaiva M.A., Perteu M., Price C., Pritchard B.L., Quail M.A.,		
RA	Rabinowitz E., Rawlins N., Rajandream M.-A., Reichard U.,		
RA	Renault H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.,		
RA	Ronning C.M., Rutter S., Salzberg S.L., Sanchez M.,		
RA	Sanchez-Parrero J.C., Saunders D., Seeger K., Smarec R., Smarec J.,		

GN	OrderedLocusNames=KLLA0A02673g;	DT	10-MAY-2005 (Tremblrel. 30, Last sequence update)
OS	Kluyveromyces lactis (Yeast).	DT	10-MAY-2005 (Tremblrel. 30, Last sequence update)
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;	DE	Likely mitochondrial ketol-acid reductoisomerase.
OC	Saccharomycetales; Saccharomycetaceae; Kluyveromyces.	GN	Name=ILV5; ORFNames=Ca019.7733;
OX	NCBI_TaxID=28985;	OS	Candida albicans SC5314.
RN	[1]	OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
RP	NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].	OC	Saccharomycetales; Mitosporic Saccharomycetales; Candida.
RC	STRAIN=CHS 2359 / IFO 1267 / NRRL Y-1140 / WM37;	OX	NCBI_TaxID=237561;
RX	PubMed=15229592; DOI=10.1038/nature02579;	RN	[1]
RA	Dufon B., Sherman D., Fischer G., Durrens P., Casaregola S.,	RP	NUCLEOTIDE SEQUENCE.
RA	Lafontaine J., de Montigny J., Marek C., Neuveglise C., Talia E.,	RC	STRAIN=SC5314;
RA	Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,	RX	PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA	Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,	RA	Jones T., Federspiel N.A., Chibana H., Dungan J., Kalman S.,
RA	Boisrame A., Boyer J., Cattolico L., Confalonieri F., de Daruvar A.,	RA	Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA	Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,	RA	Davis R.W., Scherz S.;
RA	Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,	RT	"The diploid genome sequence of Candida albicans.";
RA	Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Muller H.,	RL	Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RA	Nicaud J.-M., Nikolski M., Oztas S., Ozier-Kalogeropoulos O.,	RN	[2]
RA	Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,	RP	NUCLEOTIDE SEQUENCE.
RA	Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,	RC	STRAIN=SC5314;
RA	Zenou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,	RA	Dungan J., Kuo A., Newport G., Lan C.-Y., Iijima C., Adegbola O.,
RA	Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,	RA	Roberts J., Persson K., Donnelly S., Favoreto S., Izung K.-W.,
RA	Wincker P., Souciet J.-L.;	RA	Jones T., Scherer S., Agabian N.;
RT	"Genome evolution in yeasts.";	RT	"Annotation of the Genome of Candida albicans.";
RL	Nature 430:35-44 (2004).	RL	Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR	EMBL; CR382121; CAH02706.1; -; Genomic DNA.	CC	-!- CAUTION: The sequence shown here is derived from an
DR	GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.	CC	EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
DR	GO; GO:0016491; F:oxidoreductase activity; IEA.	CC	preliminary data.
DR	GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.	DR	EMBL; AACQ01000112; BAK94923.1; -; Genomic_DNA.
DR	InterPro; IPR000506; ACh_isomrdctse.	KW	Isomerase.
DR	Pfam; PF01450; ILVC; 1.	SQ	SEQUENCE 400 AA; 44848 MW; ACD3162D05078D81 CRC64;
DR	TIGRFAMs; TIGR00465; ilvC; 1.	Query Match	72.9%; Score 1526.5; DB 2; Length 400;
KW	Complete proteome.	Best Local Similarity	73.8%; Pred. No. 3.8e-101;
SQ	SEQUENCE 397 AA; 44189 MW; 7634BEC037ABAA9B CRC64;	Matches	296; Conservative 49; Mismatches 53; Indels 3; Gaps 3;
QY	11 RPARQL-----ATPAVORSSFAAASVMVRAATKAAVAPQ-QQIRGVKTMDFAGHKEQV 64	QY	1 MSAGFSAKALRPMARQLATPAVQRRSFVA-ASSVMVRAATKAAVAPQ-QQIRGVKTMDF 58
DB	3 RQARQLIANSRVITAKRAISFAARQSTVSGLRSTAFASKPLVATRGIKQINFGVEETV 62	DB	1 MSFRITTSMEARLATAKATLSKRTFSLLANATRYTAASSAAKAMTPITSIRGVKTING 60
QY	65 WERADPFKEKLEFYKDDTLALIGYSGQGGQGLNRDNLNGLNVIIGVRKDGKSKDAVQD 124	QY	59 GHKEQWERADWPCKLLEYFKDDTLALIGYSGQGGQGLNRDNLNGLNVIIGVRKDGKSW 118
DB	63 YERADWPTEKLLQYFKDDTLALIGYSGQGGQGLNRDNLNGLNVIIGVRKNGASWKAIED 122	DB	61 GTEEVVHERADWPCKERLLDYFKNDTFALITGYSGQGGQGLNRDNLNGLNVIIGVRK-GSSW 119
QY	125 GWTPGKMLFVDEAISRGTIVMNLSDAAQSETWPAKPOITKGKTLYFSGHSPVFKDL 184	QY	119 KDAVDGWPVGNLFEVDEAISRGTIVMNLSDAAQSETWPAKPOITKGKTLYFSGHGS 178
DB	123 GWVPGENLFDVNEAVQGTIVMNLSDAAQSETWSSLLKPLLTKGKTLYFSGHSPVFKDL 182	DB	120 EAAVEDGWVGENLFEVDEAISRGTIIMDLLSDAAQSETWFFHIKPOLTEGKTLYFSGHGS 179
QY	185 TKVEVPTDVIILCAPKSGRTVRSIFREGRGINSFVAVQDVYTGAEAEKAIALGVAIGS 244	QY	179 PVFKDLTKVEVPTDVIILCAPKSGRTVRSIFREGRGINSFVAVQDVYTGAEAEKAIAL 238
DB	183 THVEPPTDVIILVAPKSGRTVRSIFKEGRGINSFVAVVNDVYTGAEAEKAAQALAVAGS 242	DB	180 PVFKDLTHVEPSPNDVILAAPKSGRTVRSIFKEGRGINSFVAVVNDVYTGAEAEKAIAM 239
QY	245 GYLKTYTFKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 304	QY	239 GVAISGYLYKTYTFKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 298
DB	243 GYVYQTFKEVNSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVEATQSL 302	DB	240 AIAISGYVYKTYTFKEVNSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNTEVE 299
QY	305 YPLIGANGMDWMYEAESTTARRGAIDWSPRFKDALKPVFNQLYDVKDQSETQSLDYSN 364	QY	299 EATQSLYPLIGANGMDWMYEAESTTARRGAIDWSPRFKDALKPVFNQLYDVKDQSETQ 358
DB	303 YPLIGYGMIDMYDACSTTARRGALDWPYTFKDALKPVFDLYESTKNGSETKRSLEFNS 362	DB	300 EATQSLYPLIGYGMIDMYDACSTTARRGALDWPYTFKDALKPVFEELYESVKNGETKR 359
QY	365 QPDYREKYEAEIEIRNLNLEIRWIRAGKAVRSIRPEN 398	QY	359 SLDYNSQPDYREKYEAEIEIRNLNLEIRWIRAGKAVRSIRPENQ 399
DB	363 QPDYREKLEAEQLIIRNMEIWKVGEVRLKURPEN 396	DB	360 SLEFNSRDYKERLEEEQLTIIRNMEIWKVGEVRLKURPENQ 400
RESULT 9		RESULT 10	
Q59WWS CANAL		Q59XR8 CANAL	
ID Q59WWS CANAL PRELIMINARY; PRT; 400 AA.		ID Q59XR8 CANAL PRELIMINARY; PRT; 400 AA.	
AC Q59WWS CANAL PRELIMINARY; PRT; 400 AA.		AC Q59XR8 CANAL PRELIMINARY; PRT; 400 AA.	
DT 10-MAY-2005 (Tremblrel. 30, Created)		DT 10-MAY-2005 (Tremblrel. 30, Created)	
DE Likely mitochondrial ketol-acid reductoisomerase.		DE Likely mitochondrial ketol-acid reductoisomerase.	


```
Db      6  SSRAMKALRTMGSRRLATRSMSVMART-TAAPSMRFPAPMTA---PLMQTRGNRVMDFA 61
Qy      59  GHKEQVWERADWPKEKLELYFKDDTLALIGYSGCHGQGLNRDNLNGLNVIIGVRKDGKSW 118
Db      62  GTKENVWERSDWPREKLVDFKNDTLAIIGYSGCHGQGLNARDQGLNVIIGVRKDGASW 121
Qy     119  KDAVODGWVCKNLFEVDEAISRGTVTMNLLSDAAQSETPALKPQITKTKTLYFSGHGS 178
Db     122  KQALTEGWVPGKTLFPVEEAIKGSIIIMNLLSDAAQSETPWKAPLITKTKTLYFSGHGS 181
Qy     179  PVFKDLTKVEVPTDVIDILCAPKSGSRTVRSLSFREGGINSFAVYQDVDTGEAEKAIAL 238
Db     182  VIFKQDKIHPKQDVIVLAPKSGSRTVRLFKEGGINSFAVYQDVDTGKAQKAIGL 241
Qy     239  GVAIGSYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVE 298
Db     242  AVAVGSGFIYQTTFKKEVSDLVGERGCLMGINGLFLAQYQVLRERGHSPSEAFNETVE 301
Qy     299  EATQSLYPLIGANGMDWMYACSTTARRGAIDWSPRFKDALKPVFNQLYSDVKGSETOR 358
Db     302  EATQSLYPLIGKGLDYMFAACSTTARRGAIDWTPRPLEANKKVLNELYDNVENGEAKR 361
Qy     359  SLDYNQSDPYREKYAEEMERINLEIWRACKAVRSRLENOK 400
Db     362  SLEYSAPNRYRELYDELEIRNLEIWKAGEVRSRLENPK 403
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RESULT 15
Q02340 YEAST
ID Q02340_YEAST PRELIMINARY; PRT; 395 AA.
AC Q02340.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Acetohydroxy-acid isomeroreductase.
GN Names=ILV5;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
RA Xie Q., Jimenez A.;
RT "Cloning and molecular analysis of two different ILV5 genes from a
RT brewing strain of Saccharomyces cerevisiae.";
RL Curr. Genet. 26:398-402(1994).
DR EMBL; S77495; AAB33578.1; -; Genomic_DNA.
DR HSSP; Q01292; IQMG.
DR Ensembl; YLR355C; Saccharomyces cerevisiae.
DR GO; GO:0004455; P:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ILVc; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
SQ SEQUENCE 395 AA; 44309 MW; 2FB8CD94FD7E2AEF CRC64;
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Query Match 71.1%; Score 1489; DB 2; Length 395;
Best Local Similarity 72.2%; Pred. No. 1.8e-98;
Matches 285; Conservative 44; Mismatches 60; Indels 6; Gaps 3;

Qy 10 LRPMAQL---ATPAVORGSFVAASNVRAATKAA--VAPTOQQIRGVKTMDFAGHKEQV 64
Db 2 LRTQAAALICNSRVWTKRTFALATRAAAYSRPAARFVKP-MVATRGLKQINFGGTVETV 60

Qy 65 WEADWPKEKLELYFKDDTLALIGYSGCHGQGLNRDNLNGLNVIIGVRKDGKSWKDAVD 124
Db 61 YERADWPREKLLNLYFKDDTFALIGYSGQGLNLRDNLNGLNVIIGVRKDGASWKAIED 120

Qy 125 GWVPGKNLFEVDRAISRGTVTMNLLSDAAQSETPALKPQITKTKTLYFSGHGSFVFKDL 184
Db 121 GWVPGQNLFSVEDAIKGNVVMNLLSDAAQSETPWTKPIKLLTKTKTLYFSGHGSFVFKDL 180
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```
Qy 185 TKVEVPTDVIDILCAPKSGSRTVRSLSFREGGINSFAVYQDVDTGEAEKAIALGVAIGS 244
Db 181 THVEPPKDLVDILVAPKSGSRTVRSLSFKEGGINSFYAVNDVTGKAHEKAQALAIVAIGS 240
Qy 245 GYLYKTTTPEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304
Db 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
Qy 305 YPLIGANGMDWMYACSTTARRGAIDWSPRFKDALKPVFNQLYSDVKGSETQRSJDYNS 364
Db 301 YPLIGKYGMDYWDACSTTARRGALDWYDFKNALKPVFQDLYESTKNGTETKRSLEFNS 360
Qy 365 QPDYREKYAEEMERINLEIWRACKAVRSRLENQ 399
Db 361 QPDYREKLEKELVTIRNMEIWKVGEVRKLRPENK 395
```

Search completed: March 22, 2006, 15:33:24
Job time : 127.94 secs

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 123.747 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248A-2
Perfect score: 2071
Sequence: 1 MLRTQARLLCNSRVITAKR.....RNMEIWKGVKVRKLRPENC 395

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	1	ILV5 YEAST
2	2066	99.8	395	2	Q02341_YEAST
3	2023	97.7	395	2	Q02340_YEAST
4	1903	91.9	399	2	Q6FXG6_CANGA
5	1799	86.9	397	2	Q6CY71_KLULA
6	1680	81.1	394	2	Q75CW4_ASHGO
7	1667	80.5	400	2	Q59WV5_CANAL
8	1665	80.4	399	2	Q6BLZ4_DEBHA
9	1663	80.3	400	2	Q59XR8_CANAL
10	1582	76.4	398	2	Q6CAF8_YARLI
11	1528.5	73.8	402	1	ILV5 NEUCR
12	1507.5	72.8	405	2	Q4HV40_GIBZE
13	1507	72.8	400	2	Q52F28_WAGGR
14	1494.5	72.2	508	2	Q4WYV4_ASPFU
15	1477	71.3	400	2	Q5BAA4_EMENI
16	1467.5	70.9	404	1	ILV5 SCHPO
17	1401.5	67.7	401	2	Q55QW8_CRYNE
18	1401.5	67.7	401	2	Q55QW8_CRYNE
19	1383.5	66.8	401	2	Q96VZ5_CRYNE
20	1256.5	60.7	625	2	Q4P572_USTWA
21	1122	54.2	352	2	Q94135_9FUNG
22	1107.5	53.5	362	2	Q5L9J3_BACFN
23	1101.5	53.2	359	2	Q8A612_BACTN
24	1099.5	53.1	347	2	Q64PT1_BACFR
25	1038	50.1	344	2	Q84TR5_ASTYP
26	505	24.4	332	1	ILVC PYRFU
27	495	23.9	332	1	ILVC PYRAB
28	485.5	23.4	333	1	ILVC AQAAE
29	484	23.4	330	1	ILVC METMP
30	478	23.1	334	1	ILVC METJA
31	478	23.1	335	1	ILVC METAC

32	473	22.8	328	1	ILVC PYRAE
33	470	22.7	337	1	ILVC CLOAB
34	468	22.6	331	1	ILVC LISIN
35	468	22.6	331	1	ILVC LISMF
36	468	22.6	335	1	ILVC SULSO
37	468	22.6	336	1	ILVC THEMA
38	467.5	22.6	341	2	Q5KWJ2_GEOKA
39	466	22.5	335	1	ILVC METMA
40	465.5	22.5	341	2	Q8RL86_BACST
41	465	22.5	331	1	ILVC LISMO
42	465	22.5	332	1	ILVC SULTO
43	461.5	22.3	336	1	ILVC1_BACCI
44	461.5	22.3	336	2	Q63DX9_BACCC
45	461	22.3	342	1	ILVC_BACSU

ALIGNMENTS

RESULT 1
ID ILV5 YEAST STANDARD; PRT; 395 AA.
AC P06168;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxyacyl reductoisomerase).
GN Name=ILV5; OrderedLocNames=YLR355C; ORFNames=L9638.7;
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_TaxID=4932;
RN [1]
RP NUCLEOTIDE SEQUENCE
RX MEDLINE=87117524; PubMed=3027658;
RA Petersen J.G.L., Holmberg S.;
RT "The ILV5 gene of Saccharomyces cerevisiae is highly expressed."
RL Nucleic Acids Res. 14:9631-9651(1986).

RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=S288C / AB972;
RX MEDLINE=97313267; PubMed=9169871;
RA Johnston M., Hillier L.W., Riles L., Albertmann K., Andre B., Ansoorge W., Benes V., Brueckner M., Delius H., Dubois E., Duesterhoeft A., Entian K.-D., Floeth M., Goffeau A., Hehling U., Heumann K., Heuss-Neitzel D., Hilbert H., Hilger F., Kleine K., Koetter P., Louis E.J., Messenguy F., Mewes H.-W., Miosga T., Moestl D., Mueller-Auer S., Nentwich U., Obermaier B., Piravandi E., Pohl T.M., Portetelle D., Purnelle B., Rechmann S., Rieger M., Rinke M., Rose M., Scharfe M., Scherens B., Scholler P., Schwager C., Schwarz S., Underwood A.P., Urrestazu L.A., Vandenbol M., Verhasselt P., Vierendeels F., Voet M., Volckaert G., Voss H., Wambutt R., Weidner E., Wedler H., Zimmermann F.K., Zollner A., Hani J., Hoheisel J.D.;
RT "The nucleotide sequence of Saccharomyces cerevisiae chromosome XII.";
RL Nature 387:87-90(1997).
RN [3]
RP PROTEIN SEQUENCE OF 166-174.
RC STRAIN=S288C;
RX MEDLINE=95203288; PubMed=7895733;
RA Garrels J.I., Futcher B., Kobayashi R., Latter G.I., Schwender B., Volpe T., Warner J.R., McLaughlin C.S.;
RT "Protein identifications for a Saccharomyces cerevisiae protein database.";
RL Electrophoresis 15:1466-1486(1994).
RN [4]
RP IDENTIFICATION OF PROBABLE N-TERMINUS.
RX MEDLINE=97121404; PubMed=8962070; DOI=10.1073/pnas.93.25.14440;
RA Shevchenko A., Jensen O.N., Podtelejnikov A.V., Sagliocco F., Wilm M., Vorm O., Mortensen P., Shevchenko P., Boucherie H., Mann M.;
RT "Linking genome and proteome by mass spectrometry: large-scale

Q8ZTE1	pyrobaculum
Q97MV0	clostridium
Q92A29	listeria in
Q71Y36	listeria mo
Q9UW9	sulfobolus
Q9WZ0	thermotoga
Q5KWJ2	geobacillus
Q8PZ26	methanosarc
Q8RL86	bacillus st
Q8Y580	listeria mo
Q971A9	sulfobolus
Q73BA1	bacillus ce
Q63DX9	bacillus ce
P37Z53	bacillus au

RT identification of yeast proteins from two dimensional gels.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:14440-14445(1996).
 CC -1- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate + NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-isoleucine from 2-oxobutanoate; step 2.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine from pyruvate; step 2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
 CC -----
 CC EMBL; X04969; CAA28643.1; -; Genomic DNA.
 DR EMBL; U19102; AAB67753.1; -; Genomic DNA.
 DR PIR; A24709; A24709.
 DR HSSP; Q01292; IQMG.
 DR IntAct; P06168; -.
 DR GeneOnline; 142419; -.
 DR SWISS-2DPAGE; P06168; YEAST.
 DR Ensembl; YLR355C; Saccharomyces cerevisiae.
 DR SGD; S000004347; ILV5.
 DR GO; GO:0042645; C:mitochondrial nucleoid; IDA.
 DR GO; GO:0005739; C:mitochondrion; IDA.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; TAS.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; TAS.
 DR GO; GO:0000002; P:mitochondrial genome maintenance; IMP.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; IlvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 DR Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
 KW Complete proteome; Direct protein sequencing; Magnesium;
 KW Mitochondrion; NADP; Oxidoreductase; transit peptide.
 FT TRANSIT 1 47 Mitochondrion (Potential).
 FT CHAIN 48 395 Ketol-acid reductoisomerase.
 FT NP BIND 84 93 NADP (Potential).
 FT REGION 363 395 Hydrophilic.
 FT ACT SITE 171 171 Potential.
 SQ SEQUENCE 395 AA; 44368 MW; D76419A6AD68E85E CRC64;
 Query Match 100.0%; Score 2071; DB 1; Length 395;
 Best Local Similarity 100.0%; Pred. No. 2.1e-141;
 Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGGLNRDNLNVIIGVRKDGASWKAALIED 120
 DB 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGGLNRDNLNVIIGVRKDGASWKAALIED 120
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 QY 181 THVEPPKDLVILVAPKSGRTVRSLFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB 181 THVEPPKDLVILVAPKSGRTVRSLFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 QY 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQQYDVLRENGHSPSEAFNVEATQSL 300
 DB 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQQYDVLRENGHSPSEAFNVEATQSL 300
 QY 301 YPLIKGYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
 DB 301 YPLIKGYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
 QY 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 DB 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395

Db 301 YPLIKGYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
 QY 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 Db 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 RESULT 2
 Q02341_YEAST PRELIMINARY; PRT; 395 AA.
 ID Q02341_YEAST PRELIMINARY; PRT; 395 AA.
 AC Q02341;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acetoxyhydroxy-acid isomerase.
 GN Name=ILV5; Synonyms=ILV5X;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 OX NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
 RA Xie Q., Jimenez A.;
 RT "Cloning and molecular analysis of two different ILV5 genes from a brewing strain of Saccharomyces cerevisiae.";
 RL Curr. Genet. 26:398-402(1994).
 DR EMBL; S77496; AAB33579.1; -; Genomic DNA.
 DR HSSP; Q01292; IQMG.
 DR Ensembl; YLR355C; Saccharomyces cerevisiae.
 DR SGD; S000004347; ILV5.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; IlvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 SQ SEQUENCE 395 AA; 44385 MW; D1D319A6A238E85E CRC64;
 Query Match 99.8%; Score 2066; DB 2; Length 395;
 Best Local Similarity 99.7%; Pred. No. 4.8e-141;
 Matches 394; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 DB 1 MLRTQARLNCNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGTVETV 60
 QY 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGGLNRDNLNVIIGVRKDGASWKAALIED 120
 DB 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGGLNRDNLNVIIGVRKDGASWKAALIED 120
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 DB 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDDAAQSETWPAIKPLLTKGKTLFSGHGFSPVKDL 180
 QY 181 THVEPPKDLVILVAPKSGRTVRSLFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 DB 181 THVEPPKDLVILVAPKSGRTVRSLFKEGRGINSYAVVNDVTGKAHKAQALAVAIGS 240
 QY 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQQYDVLRENGHSPSEAFNVEATQSL 300
 DB 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQQYDVLRENGHSPSEAFNVEATQSL 300
 QY 301 YPLIKGYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
 DB 301 YPLIKGYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
 QY 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 DB 361 QPDYREKLEKELDTIRNMEIWKVGKVRKLRPENQ 395
 RESULT 3
 Q02340_YEAST

Q02340 YEAST PRELIMINARY; PRT; 395 AA.
 AC Q02340;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Acetohydroxy-acid isomeroreductase.
 GN Name=ILV5G;
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 NCBI_TaxID=4932;
 RN [1]
 RP NUCLEOTIDE SEQUENCE
 RA MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;
 RA Xie Q., Jimenez A.;
 RT "Cloning and molecular analysis of two different ILV5 genes from a
 RT brewing strain of Saccharomyces cerevisiae.";
 RL Curr. Genet. 26:398-402(1994).
 DR EMBL; S77495; AAB33578.1; -; Genomic_DNA.
 DR HSSP; Q01292; 10MG.
 DR Ensembl; YLR355C; Saccharomyces cerevisiae.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; ilvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 DR SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2ABF CRC64;
 SQ
 Query Match 97.7%; Score 2023; DB 2; Length 395;
 Best Local Similarity 97.0%; Pred. No. 6.2e-138;
 Matches 383; Conservative 9; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGVETV 60
 Db 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGGVETV 60
 Qy 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWKAIED 120
 Db 61 YERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWKAIED 120
 Qy 121 GWVPGKQLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGSPVPKDL 180
 Db 121 GWVPGKQLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGSPVPKDL 180
 Qy 181 THVEPPKDLVDILVAPKSGRTVRSFLKEGGINSSYAVVNDVTGKAHEKAQALAVAIGS 240
 Db 181 THVEPPKDLVDILVAPKSGRTVRSFLKEGGINSSYAVVNDVTGKAHEKAQALAVAIGS 240
 Qy 241 GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSFAFNETVEEATQSL 300
 Db 241 GYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSFAFNETVEEATQSL 300
 Qy 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVFQDLVYESTKNGTETKRSLEFNS 360
 Db 301 YPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVFQDLVYESTKNGTETKRSLEFNS 360
 Qy 361 QPDYREKLEKELDTIRNMEIWKVGEVVKLRPENQ 395
 Db 361 QPDYREKLEKELDTIRNMEIWKVGEVVKLRPENK 395
 RESULT 4
 Q6FXG6 CANGA
 ID Q6FXG6 CANGA PRELIMINARY; PRT; 399 AA.
 AC Q6FXG6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Candida glabrata strain CBS138 chromosome B complete sequence.
 GN OrderedLocNames=CAGL0B03047g;
 OS Candida glabrata (Yeast) (Torulopsis glabrata).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

NCBI_TaxID=5478;
 OX [1]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
 RC STRAIN=ATCC 2901 / CBS 138;
 RX PubMed=15229592; DOI=10.1038/nature02579;
 RA Dujon B., Sherman D., Fischer G., Durans P., Casaregola S.,
 RA Lafontaine I., de Montigny J., Marck C., Neuvéglise C., Talia E.,
 RA Goffard N., Frangeul L., Aigle M., Anthouard V., Babour A., Barbe V.,
 RA Barnay S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
 RA Boissame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
 RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
 RA Hantraye F., Hennequin C., Jauniaux N., Joyet P., Kachouri R.,
 RA Kerrest A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
 RA Niclaud J.-M., Nikolski M., Ostas S., Ozier-Kalogeropoulos O.,
 RA Pellens S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
 RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
 RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
 RA Bouchier C., Caudron B., Scarpelli C., Gallardin C., Weissenbach J.,
 RA Wincker P., Souciet J.-L.;
 RT "Genome evolution in yeasts.";
 RL Nature 430:35-44(2004).
 DR EMBL; CR380948; CAG58005.1; -; Genomic DNA.
 DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR Pfam; PF01450; ilvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 DR Complete proteome.
 KW SEQUENCE 399 AA; 44568 MW; E2241C86A034D728 CRC64;
 SQ
 Query Match 91.9%; Score 1903; DB 2; Length 399;
 Best Local Similarity 89.5%; Pred. No. 3e-129;
 Matches 358; Conservative 26; Mismatches 10; Indels 6; Gaps 2;
 Qy 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAA-----RVKPMITTRGLKQINFGG 55
 Db 1 MLRTQAAALICNSRVITAKRTFALATRAAAYSRPAA-----RVKPMITTRGLKQINFGG 59
 Qy 56 TVETVYERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWK 115
 Db 60 TVETVYERADWPREKLLDYFKNDTFALIGYSGQYGGQGLNLRDNLNGLNVLIGVRKDGASWK 119
 Qy 116 AATDGWVPGKQLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGFSFP 175
 Db 120 AATDGWVPGKQLFTVEDAIKRGSYVMNLLSAAQSETWPAIKPLLTGKTLTFSHGFSFP 179
 Qy 176 VFQDLTHVEPPKDLVDILVAPKSGRTVRSFLKEGGINSSYAVVNDVTGKAHEKAQALA 235
 Db 180 VFQDLTHVEPPKDLVDILVAPKSGRTVRSFLKEGGINSSYAVVNDVTGKAHEKAQALA 239
 Qy 236 VAIGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSFAFNETVEE 295
 Db 240 VAVGSGYVYQTTFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSFAFNETVEE 299
 Qy 296 ATQSLYPLIGKGYMDYDACSTTARRGALDWYPIFKNALKPVFQDLVYESTKNGTETKRS 355
 Db 300 ATQSLYPLIGKGYMDYDACSTTARRGALDWYPIFKDALKPVFQDLVYESTKNGTETKRS 359
 Qy 356 LEFNSQPDYREKLEKELDTIRNMEIWKVGEVVKLRPENQ 395
 Db 360 LEFNSQPDYREKLEKELDTIRNMEIWRVGEVVKLRPENQ 399
 RESULT 5
 Q6CY71 KUULA
 ID Q6CY71 KUULA PRELIMINARY; PRT; 397 AA.
 AC Q6CY71;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Kluyveromyces fragilis strain NRRL Y-1140 chromosome A of strain NRRL Y-1140 of Kluyveromyces fragilis.

```

GN OrderedLocuNames=KL0A0A02673g;
OS Kluyveromyces lactis (Yeast);
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=CBS 2359 /IFO 1267 /NRRL Y-1140 /WM37;
RX PubMed=15229592; DOI=10.1038/nature02579;
RA Lafontaine I., de Montigny J., Marck C., Neugebäude C., Tallia E.,
RA Goffard N., Frangeul L., Aigle M., Anthonard V., Babour A., Barbe V.,
RA Barney S., Blanchin S., Beckerich J.-M., Beyne E., Bleykasten C.,
RA Boisrame A., Boyer J., Cattolico L., Confanioli F., de Daruvar A.,
RA Despons L., Fabre E., Fairhead C., Ferry-Dumazet H., Groppi A.,
RA Hantaye F., Henneguen C., Jauniaux N., Joyet P., Kachouri R.,
RA Kersat A., Koszul R., Lemaire M., Lesur I., Ma L., Müller H.,
RA Nicoud J.-M., Nikolski M., Orlas S., Ozier-Kalogeropoulos O.,
RA Pellenz S., Potier S., Richard G.-F., Straub M.-L., Suleau A.,
RA Swennen D., Tekala F., Wesolowski-Louvel M., Westhof E., Wirth B.,
RA Zeniou-Meyer M., Zivanovic Y., Bolotin-Fukuhara M., Thierry A.,
RA Bouchier C., Caudron B., Scarpelli C., Gaillardin C., Weissenbach J.,
RA Winkler P., Souciet J.-L.;
RT "Genome evolution in yeasts.";
RL Nature 430:35-44 (2004).
DR EMBL; CR382121; CAH02706.1; -; Genomic DNA.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
KW Complete proteome.
SQ SEQUENCE 397 AA; 44189 MW; 7634BEC037ABAA9B CRC64;

Query Match 86.9%; Score 1799; DB 2; Length 397;
Best Local Similarity 85.9%; Pred. No. 1e-121;
Matches 340; Conservative 23; Mismatches 31; Indels 2; Gaps 1;

QY 1 MLRTQAQLNSRVITAKETPALATAAAYS--RPAARFVKPMITRGLKQINFGTVE 58
DB 1 MFQAARQLIANSRVITAKRAISFAARQSTVSLRSTAFASKPLATRGIKQINFGVBE 60
QY 59 TVYERADWPPEKLLDYFKNDTFALIGYSGQYQGGNLNRDNLNGLNVIIGVRKDGASWKA 118
DB 61 TVYERADWPPEKLLDYFKNDTFALIGYSGQYQGGNLNRDNLNGLNVIIGVRKDGASWKA 120
QY 119 EDGWVPGKLTFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPK 178
DB 121 EDGWVPGKLTFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPK 180
QY 179 DLTHVPPKDLVDILVAPKSGRTVRSFLKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 238
DB 181 DLTHVPPKDLVDILVAPKSGRTVRSFLKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 240
QY 239 GSGYVYQTTFERVNSDLGERCLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEATQ 298
DB 241 GSGYVYQTTFERVNSDLGERCLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEATQ 300
QY 299 SLVPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEF 358
DB 301 SLVPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEF 360
QY 359 NSQPDYREKLEKELDTIRNMEIWKVKEVRKLRPEN 394
DB 361 NSQPDYREKLEKELDTIRNMEIWKVKEVRKLRPEN 396

RESULT 6
Q75CW4 ASHGO
ID Q75CW4_ASHGO PRELIMINARY; PRT; 394 AA.
AC Q75CW4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

us-10-797-248a-2.rup

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
ACLI98Wp.
GN Name=ACLI98W;
OS Ashbya gossypii (Yeast) (Bremothecium gossypii).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Bremothecium.
OX NCBI_TaxID=33169;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=ATCC 10895;
RX PubMed=15001715; DOI=10.1126/science.1095781;
RA Dietrich F.S., Voegeli S., Brachat S., Lerch A., Gates K., Steiner S.,
RA Mohr C., Poehmann R., Luedi P., Choi S., Wing R.A., Flavler A.,
RA Gaffney T.D., Philippsen P.;
RT "The Ashbya gossypii genome as a tool for mapping the ancient
Saccharomycetes cerevisiae genome.";
RL Science 304:304-307 (2004).
DR EMBL; AR016816; RAS51030.1; -; Genomic DNA.
DR AGD; ACL198W; -.
DR GO; GO:0004455; F:keto-acid reductoisomerase activity; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
DR InterPro; IPR000506; ACh_isomrdctse.
DR Pfam; PF01450; ILVC; 1.
DR TIGRFAMs; TIGR00465; ilvC; 1.
KW Complete proteome.
SQ SEQUENCE 394 AA; 43675 MW; 15A4E4FB942ACDA3 CRC64;

Query Match 81.1%; Score 1680; DB 2; Length 394;
Best Local Similarity 81.5%; Pred. No. 4.1e-113;
Matches 317; Conservative 32; Mismatches 28; Indels 12; Gaps 2;

QY 18 AKRTFALATRAAY-----SRPAARFVK-----PMITRGLKQINFGTVEYERAD 65
DB 5 AGRQMIAGTRAAAWRALSGARARAAWPPVRSARAAAPVQSGRGVKQISFGTPTVEYERAD 64
QY 66 WPREKLLDYFKNDTFALIGYSGQYQGGNLNRDNLNGLNVIIGVRKDGASWKAIEDGWVPG 125
DB 65 WPREKLLDYFKNDTFALIGYSGQYQGGNLNRDNLNGLNVIIGVRKDGASWKAIEDGWVPG 124
QY 126 KNLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLTYFSGHSPVPKDLTHVEP 185
DB 125 ENLFDVWEAVERGTIVMNLSDAAQSETWPTPLLTGKTLTYFSGHSPVPKDLTHVEP 184
QY 186 PKDLVDILVAPKSGRTVRSFLKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 245
DB 185 PKDLVDILVAPKSGRTVRSFLKEGRGINSSYAVVNDVTGKAHEKAQALAVAI 244
QY 246 TTFEREVNSDLGERCLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLVPLIG 305
DB 245 TTFEREVNSDLGERCLMGGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLVPLIG 304
QY 306 KYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNQPDYR 365
DB 305 KHGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNQPDYR 364
QY 366 EKLEKELDTIRNMEIWKVKEVRKLRPEN 394
DB 365 DKLEAELOITRMEIWKVKEVRKLRPEN 393

RESULT 7
Q59WWS CANAL
ID Q59WWS CANAL PRELIMINARY; PRT; 400 AA.
AC Q59WWS;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Likely mitochondrial ketol-acid reductoisomerase.
GN Name=ILV5; ORFNames=CaO19.7733;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
```


FT	CHAIN	27	402	Ketol-acid reductoisomerase.		
FT	NP BIND	90	99	NADP (Potential).		
FT	ACT SITE	177	177	Potential.		
FT	CONFLICT	358	358	T->R (in Ref. 1).		
FT	CONFLICT	392	393	Missing (in Ref. 1).		
FT	SEQUENCE	402 AA;	44623 MW;	246F795898D2A174 CRC64;		
Query Match						
Best Local Similarity 74.1%; Score 1528.5; DB 1; Length 402;						
Matches 297; Conservative 39; Mismatches 50; Indels 15; Gaps 4						
QY	4	TOAARLINCNSRVITA--KRTPF---ALATRAA----	AYSPPAARFVKPMITTRGLKQINFG	54		
DB	7	TKALRPLARQLATPAVQRRTFVAASAVRASVAVKAVAAPARQOV-----	RGVKTMDFA	60		
QY	55	GTVTVTVERADWPPEKLLDYFKNDTFALTCYGSOGVCGGLNLRDGLNGLVIVGRVKGDSW	114			
DB	61	GKHEVHERADWPAEKLLDYFKNDTTLALIGYSGHGQGLNLRDGLNGLVIVGRVKGKSW	120			
QY	115	KAALTEGWPVCKNLTFTVEDAIKRGSVYVNMLLSDAAQSETPAIKPLLTKGKTLFVSHGFS	174			
DB	121	EDAQDQWVCKNLFVDEAIKRGTVVNMLLSDAAQSETPAIKPLLTKGKTLFVSHGFS	180			
QY	175	PVFKDLTHVPPKDLVDILVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHKAQAL	234			
DB	181	PVFKDLTKVEPTDVIDLVAPKSGRTVRSFLFKEGRGINSYAVVNDVTGKAHKAQAL	240			
QY	235	AVATGSGVYVQTTFERVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNVTVE	294			
DB	241	GVAVGSGLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNVTVE	300			
QY	295	EATOSLPLIGKYGMDVYDACSTTARRGALDWYPIFKNALKVPQDLYESTKNGCTETKR	354			
DB	301	EATOSLPLIGANGMDVYDACSTTARRGALDWYPIFKNALKVPQDLYESTKNGCTETKR	360			
QY	355	SLEFNSPDYREKLEKELDTIRNMEIWKYGVKEVKLRLENQ	395			
DB	361	SLEFNSPDYRERYEAELDRNLEWTRAGKAVSLRPNQ	401			
RESULT 12						
Q4HY40 GIBZE PRELIMINARY; PRT; 405 AA.						
Q4HY40:						
AC	Q4HY40	GIBZE	PRELIMINARY;	PRT; 405 AA.		
DT	13-SEP-2005	(TrEMBLrel. 31, Created)				
DT	13-SEP-2005	(TrEMBLrel. 31, Last sequence update)				
DE	ILV5 NEUCR	Ketol-acid reductoisomerase, mitochondrial				
DE	acid reductoisomerase)	(Alpha-keto-beta-hydroxylacil				
GN	ORFNames=FG10118.1;					
OS	Gibberella zeae PH-1.					
OC	Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;					
OC	Hypocorymbidae; Hypocreales; Nectriaceae; Gibberella.					
OX	NCBI_TaxID=229533;					
RN	[1]					
RP	NUCLEOTIDE SEQUENCE.					
RC	STRAIN=PH-1;					
RA	Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,					
RA	Arachchi H.M., Barna N., Bastien V., Bloom T., Boguslavsky L.,					
RA	Boukhaltier B., Butler J., Calvo S.E., Camarata J., Chang J.,					
RA	Chepel Y., Collymore A., Cook A., Cooke P., Corum B., Dearellano K.,					
RA	Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,					
RA	Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,					
RA	Gardyna S., Gnerre S., Graham L., Gordon-Pierre N., Hafez N.,					
RA	Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,					
RA	Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,					
RA	Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,					
RA	Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,					
RA	Mathews C., Maucelli E., McCarthy M., Meldrum J., Meneus L.,					
RA	Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,					
RA	Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,					
RA	Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,					

QY 241 GYVYQTTTFEVRNSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSL 300
 DB 245 GYLKATTFEKEVYSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSL 304
 QY 301 YPLIKGYMDYMDACSTTARRGALDWYPIFKNALKPVDLYSTKNGTETKRSLEFNS 360
 DB 305 YPLIGANGMDWYEAACSTTARRGALDWYPIFKNALKPVDLYSTKNGTETKRSLEFNS 364
 QY 361 QPDYREKLEKELDIRNMEIWKVKEVRLRPENQ 395
 DB 365 QPDYREKYEAEEMERINLEIWRAGKAVRSLRPENQ 399
 RESULT 14
 Q4WY4 ASPFU
 ID Q4WY4 ASPFU PRELIMINARY; PRT; 508 AA.
 AC Q4WY4;
 DT 13-SEP-2005 (TremBLrel. 31, Created)
 DT 13-SEP-2005 (TremBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TremBLrel. 31, Last annotation update)
 DE Ketol-acid reductoisomerase.
 GN ORFNames=Afu3g14490;
 OS Aspergillus fumigatus Af293.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxID=330879;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Af293;
 RA Niernan W., Pain A., Anderson M.J., Wortman J., Kim H., Stanley,
 RA Arroya J., Berrian M., Abe K., Archer D.B., Bermejo C., Bennett J.,
 RA Bowyer P., Chen D., Collins M., Coulson R., Davies R., Dyer P.S.,
 RA Farman M., Fedorova N., Fedorova N., Feldblyum T.V., Fischer R.,
 RA Foster N., Fraser A., Garcia J.L., Garcia M.J., Goble A.,
 RA Goldman G.H., Goni K., Griffith-Jones S., Humphrey S., Jimenez J.,
 RA Haas H., Harris D., Horiuchi H., Huang J., Humphrey S., Jimenez J.,
 RA Keller N., Khouri H., Kitamoto K., Kobayashi T., Kulkarni R.,
 RA Kumagai T., Lafton A., Lage J.-F., Li W., Lord A., Lu C.,
 RA Majoros W.H., May G.S., Miller B.L., Mohamoud Y., Molina M., Monod M.,
 RA Mouyna I., Mulligan S., Murphy L., O'Neil S., Paulsen I.,
 RA Peralva M.A., Perteau M., Price C., Pritchard B.L., Quail M.A.,
 RA Rabinowitsch E., Rawlins N., Rajandream M.-A., Reichard U.,
 RA Renauld H., Robson G.D., Rodriguez de Cordoba S., Rodriguez-Pena J.M.,
 RA Ronning C.M., Ruter S., Salzberg S.L., Sanchez M.,
 RA Sanchez-Ferrero J.C., Saunders D., Seeger K., Squares S.,
 RA Takeuchi M., Tekai F., Turner G., Vazquez de Aldana C.R., Weidman J.,
 RA White O., Woodward J., Yu J.-H., Fraser C., Galagan J.E., Asai K.,
 RA Machida M., Hall N., Barrell B., Denning D.W.,
 RA "Genomic sequence of the pathogenic and allergenic filamentous fungus
 Aspergillus fumigatus.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 CC EMBL; AAHP01000002; EAL92139.1; -; Genomic_DNA.
 DR isomerase.
 KW SEQUENCE 508 AA; 56353 MW; 09C99AB04D9D92EC CRC64;
 Query Match 72.2%; Score 1494.5; DB 2; Length 508;
 Best Local Similarity 71.9%; Pred. No. 1.5e-99;
 Matches 281; Conservative 46; Mismatches 61; Indels 3; Gaps 1;
 QY 5 QARALICNSRVITAKRTFFALATRAAAYSRPAARFVKPMITTRGLKQINFGTGVYVERA 64
 DB 120 RALRL---ARVAAPRTVISAALPRPALAKAATRAAATAVPVGVKTIATFADSKETVYERA 176
 QY 65 DWPREKLLDYKNDTFALIGYSGYCGQLNRDNLNGLNVIYVRKDGASWKAIEDGWVP 124
 DB 177 DWPREKLOEYFKNDTLALIGYSGYCGQLNRDNLNGLNVIYVRKDGASWKAIEDGWIP 236
 QY 125 GKNLFTVEDALKRGSYVWNLSDAAQSETWPAIKTLTKGTLTYFSHGSPVFKDLTHVE 184
 DB 237 GKNLFDITEAVQKGTIVWNLSDAAQSETWPTLTKLTKGTLTYFSHGSPVFKELTKVD 296

QY 185 PPKDLVDILVAPKSGRTVRSFLPKBGRGINSSVAVMNDVTGKAHEKAQALAVAGSYVY 244
 DB 297 VPKDVVDILVAPKSGRTVRSFLPKBGRGINSSVAVMNDVTGKAHEKAQALAVAGSYVY 356
 QY 245 QTTTFEVRNSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSLYPLI 304
 DB 357 ETTFEKEVYSDLYGERCLMGHGMFLAQYDVLRENGHSPSEAFNVEATQSLYPLI 416
 QY 305 GYKGYMDYMDACSTTARRGALDWYPIFKNALKPVDLYSTKNGTETKRSLEFNSQPDY 364
 DB 417 GANGMDWYEAACSTTARRGALDWYPIFKNALKPVDLYSTKNGTETKRSLEFNSQKDY 476
 365 REKLEKELDIRNMEIWKVKEVRLRPENQ 395
 477 REKYEKEMQDIRDLEIWRAGKAVRSLRPENQ 507
 RESULT 15
 Q5BAA4 EMENI
 ID Q5BAA4 EMENI PRELIMINARY; PRT; 400 AA.
 AC Q5BAA4;
 DT 10-MAY-2005 (TremBLrel. 30, Created)
 DT 10-MAY-2005 (TremBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TremBLrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=AN2526.2;
 OS Aspergillus nidulans FGSC A4.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; Emericella.
 OX NCBI_TaxID=227321;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=FGSC A4;
 RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
 RA Arachchi H.M., Barna N., Bastien V., Bloom T., Boguvalskiy L.,
 RA Boukigalter B., Butler J., Calvo S.E., Camarata J., Chang J.,
 RA Choepel Y., Collymore A., Cooke K., Cooke P., Corum B., Dearellano K.,
 RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
 RA Erickson J., Faro S., Ferreira P., FitzGerald M., Gage D., Galagan J.,
 RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamal M., Kamat A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt R., Maclean C., Macdonald P., Major J., Manning J.,
 RA Matthews C., Mauceli B., McCarthy M., Meldrim J., Meneus L.,
 RA Mihova T., Mlenga V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neil D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Rachupka A., Ramasamy U., Raymond C., Retta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schuback R., Seaman S., Severy P., Smirnov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talanas J., Tesfaye S., Theodore J., Topham K., Travers M.,
 RA Vassiliev H., Venkataraman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek L., Zimmer A., Zody M.,
 RA Lander E.;
 RT "Genome Sequence of Aspergillus nidulans.";
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AACD01000043; EAA64631.1; -; Genomic DNA.
 DR GO; GO:0004455; F:ketol-acid reductoisomerase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.
 DR InterPro; IPR000506; ACh_isomcdctse.
 DR DR PF01450; ILVC; 1.
 DR TIGRFAMs; TIGR00465; ilvc; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 400 AA; 44354 MW; F76A7F2A5AB65FA1 CRC64;
 Query Match 71.3%; Score 1477; DB 2; Length 400;
 Best Local Similarity 71.1%; Pred. No. 2e-98;
 Matches 278; Conservative 49; Mismatches 62; Indels 2; Gaps 1;

QY 5 QARALICNSRVITAKRTFFALATRAAAYSRPAARFVKPMITTRGLKQINFGTGVYVERA 64

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:27 ; Search time 125.313 Seconds
(without alignments)
2252.046 Million cell updates/sec

Title: US-10-797-248a-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRAGKRSIRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2069	99.2	402	1	ILV5_NEUCR
2	1860	89.2	400	2	Q52F28_MAGGR
3	1819.5	87.2	408	2	Q4HY40_GIBZE
4	1639	78.6	505	2	Q4WY4 ASPFU
5	1611	77.2	400	2	Q5BAA4_EWENI
6	1560.5	74.8	398	2	Q6CAP8_YARLI
7	1542	73.9	399	2	Q6BLZ4_DEBHA
8	1539.5	73.8	400	2	Q59WWS_CANAL
9	1535.5	73.6	400	2	Q59XR8_CANAL
10	1524	73.1	397	2	Q6CV71_KLULA
11	1508.5	72.3	395	1	ILV5_YEAST
12	1506.5	72.2	395	2	Q02341_YEAST
13	1500.5	71.9	399	2	Q6FAG6_CANGA
14	1494.5	71.6	404	1	ILV5_SCHPO
15	1479.5	70.9	395	2	Q02340_YEAST
16	1466.5	70.3	394	2	Q75CW4_ASHGO
17	1434.5	68.8	401	2	Q5KQW8_CRYNE
18	1434.5	68.8	401	2	Q5KFA0_CRYNE
19	1417.5	68.0	401	2	Q96VZ5_CRYNE
20	1232	59.1	625	2	Q4P572_USTWA
21	1099	52.7	352	2	Q94135_PIRYMES
22	1086.5	52.1	362	2	Q519J3_BACTEROIDES
23	1084.5	52.0	347	2	Q64PT1_BACFR
24	1075.5	51.6	359	2	Q8A612_EACTN
25	1071	51.3	344	2	Q847R5_ASTYP
26	510.5	24.5	341	2	Q5KRWJ2_GEOKA
27	507.5	24.3	341	2	Q8RL86_BACST
28	497	23.8	333	1	ILV5_AQUAE
29	486	23.6	332	1	ILV5_PFRAB
30	486	23.3	332	1	ILV5_PFRAB
31	484.5	23.2	331	1	ILV5_LISIN

32 484.5 23.2 331 1 ILV5_LISINP
33 483 23.2 342 1 ILV5_BACSU
34 480.5 23.0 331 1 ILV5_LISMO
35 472.5 22.7 326 1 ILV5_METKA
36 470 22.5 335 1 ILV5_METAC
37 470 22.5 342 2 Q65GF7_BACLD
38 469.5 22.5 381 1 ILV5_PEA
39 469 22.5 328 1 ILV5_PYRAE
40 469 22.5 332 1 ILV5_GLOVI
41 466 22.3 578 2 Q65XK0_ORYSA
42 465 22.3 591 1 ILV5_ARATH
43 463 22.2 335 1 ILV5_SULSO
44 463 22.2 337 1 ILV5_CIOAB
45 463 22.2 341 2 Q5WEN2_BACSK

ALIGNMENTS

RESULT 1

ILV5_NEUCR STANDARD; PRT; 402 AA.
AC P38674: Q7RVD5: Q8X019;
DT 01-FEB-1995 (Rel. 31, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ketol-acid reductoisomerase, mitochondrial precursor (EC 1.1.1.86)
DE (Acetohydroxy-acid reductoisomerase) (Alpha-keto-beta-hydroxylacil reductoisomerase).
GN Name=ilv-2; ORFNames=B11H24.150, NCU03608;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93013010; PubMed=1398116; DOI=10.1016/0378-1119(92)90018-K;
RA Sista H., Bowman B.;
RT "Characterization of the ilv-2 gene from Neurospora crassa encoding alpha-keto-beta-hydroxylacil reductoisomerase.";
RL Gene 120:115-118(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22542210; PubMed=12655011; DOI=10.1093/nar/gkg293;
RA Mannhaupt G., Montrone C., Haase D., Mewes H.-W., Altmann V.,
Hoheisel J.D., Fartmann B., Nyakatura G., Kempken F., Maier J.,
Schulte U.;
RT "What's in the genome of a filamentous fungus? Analysis of the Neurospora genome sequence.";
RL Nucleic Acids Res. 31:1944-1954(2003).
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=74-OR23-1A / FGSC 987;
RX MEDLINE=22598136; PubMed=12712197; DOI=10.1038/nature01554;
RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D., Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehman B., Elkins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M., Qui D., Iankiev P., Bell-Pedersen D., Nelson M.A., Werner-Washburne M., Selitrennikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U., Kothe G.O., Jedd G., Mewes H.-W., Staben C., Marcotte E., Greenberg D., Roy A., Foley K., Naylor J., Stange-Thomann N., Barrett R., Gnerre S., Kamal M., Kanvasek M., Rasmussen C., Mettenberg R.L., Perkins D.D., Kroken S., Cogoni C., Macino G., Catchen D.E.A., Li W., Pratt R.J., Osmari S.A., deSouza C.P.C., Glass N.I., Orbach M.J., Berglund J.A., Voelker R., Yarden O., Plamann M., Seiler S., Dunlap J.C., Radford A., Aramayo R., Natvig D.O., Alex L.A., Mannhaupt G., Ebbel D.J., Freitag M., Paulsen I., Sachs M.S., Lander E.S., Nusbaum C., Birren B.W.;
RT "The genome sequence of the filamentous fungus Neurospora crassa.";
RL Nature 422:859-868(2003).
CC -!- CATALYTIC ACTIVITY: (R)-2,3-dihydroxy-3-methylbutanoate + NADP(+) ->

Q7LY36 listeria mo
P37253 bacillus su
Q8Y560 listeria mo
Q8TX44 methanopyru
Q8TJJ4 methanosarc
Q85G17 bacillus li
Q82043 pisum sativ
Q8ZTEL pyrobaculum
Q7NH80 gloeobacter
Q65XK0 oryza sativ
Q05Y58 arabidopsis
Q9UW9 culicoides
Q97MVO clostridium
Q5WEN2 bacillus cl

CC = (S)-2-hydroxy-2-methyl-3-oxobutanoate + NADPH.
 CC -1- CATALYTIC ACTIVITY: (2R,3R)-2,3-dihydroxy-3-methylpentanoate +
 CC NADP(+) = (S)-2-hydroxy-2-ethyl-3-oxobutanoate + NADPH.
 CC -1- COFACTOR: Magnesium.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-isoleucine biosynthesis; L-
 CC isoleucine from 2-oxobutanoate; step 2.
 CC -1- PATHWAY: Amino-acid biosynthesis; L-valine biosynthesis; L-valine
 CC from pyruvate; step 2.
 CC -1- SUBCELLULAR LOCATION: Mitochondrial.
 CC -1- SIMILARITY: Belongs to the ketol-acid reductoisomerase family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC EMBL; M84189; AAB00797.1; -; Genomic DNA.
 CC EMBL; AL670005; CAD21284.1; -; Genomic DNA.
 CC EMBL; ABX01000270; EAA32099.1; -; Genomic DNA.
 CC PIR; JC1428; JC1428.
 CC HSSP; O9HVA2; 1NP3.
 CC InterPro; IPR000506; ACh_isomrdctse.
 CC Pfam; PF01450; ilvC; 1.
 CC TIGRFAMs; TIGR00465; ilvC; 1.
 CC Amino-acid biosynthesis; Branched-chain amino acid biosynthesis;
 CC Magnesium; Mitochondrion; NADP; Oxidoreductase; Transist peptide.
 CC TRANSIT 1 26 Mitochondrion (Potential).
 CC CHAIN 27 402 Ketol-acid reductoisomerase.
 CC ACT_SITE 90 99 NADP (potential).
 CC FT AC_SITE 177 177 Potential.
 CC FT CONFLICT 358 358 T -> R (in Ref. 1).
 CC FT CONFLICT 392 393 Missing (in Ref. 1).
 CC SEQUENCE 402 AA; 44623 MW; 246795898D2A174 CRC64;
 CC -----
 CC Query Match 99.2%; Score 2069; DB 1; Length 402;
 CC Best Local Similarity 99.3%; Pred. No. 3e-138;
 CC Matches 399; Conservative 0; Mismatches 1; Indels 2; Gaps 1;
 CC
 CC QY 1 MAARNCTKALPLARQLATPAVQRRTFVAASAVRASVAVKAAAPARQOVRGVTMDFA 60
 CC Db 1 MAARNCTKALPLARQLATPAVQRRTFVAASAVRASVAVKAAAPARQOVRGVTMDFA 60
 CC
 CC QY 61 GHKEEVRADWPAEKLLDYFKNDTLALGYSGQHGQGLNRDNLNIVGVRKNGKSW 120
 CC Db 61 GHKEEVRADWPAEKLLDYFKNDTLALGYSGQHGQGLNRDNLNIVGVRKNGKSW 120
 CC
 CC QY 121 EDIAQDQGWVPGKMLFDVDSIAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
 CC Db 121 EDIAQDQGWVPGKMLFDVDSIAISRGTTVMNLLSDAAQSETWPHIKPQITKGKTLYFSHGFS 180
 CC
 CC QY 181 PVFKDLTKVEPTDNDVILVAPKSGRTVRSLPREGRGINSFVAVYQDVTGKAKEKAVAL 240
 CC Db 181 PVFKDLTKVEPTDNDVILVAPKSGRTVRSLPREGRGINSFVAVYQDVTGKAKEKAVAL 240
 CC
 CC QY 241 GVAVSGLYLYETTFEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHSPSEAFNETVE 300
 CC Db 241 GVAVSGLYLYETTFEKEVYSDLYGERGLMGHGMFLAQYEVLRERGHSPSEAFNETVE 300
 CC
 CC QY 301 EATQSLYPLIAGHMDMWFDACTTARRGAIDWTPKFKDALKPVFNLLYDSVKNRGERK 360
 CC Db 301 EATQSLYPLIAGHMDMWFDACTTARRGAIDWTPKFKDALKPVFNLLYDSVKNRGERK 360
 CC
 CC QY 361 SLEYNQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
 CC Db 361 SLEYNQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 402
 CC
 CC RESULT 2
 CC Q52F28_MAGGR
 CC ID Q52F28_MAGGR PRELIMINARY; PRT; 400 AA.
 CC AC Q52F28;
 CC DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=MG01808.4; 70-15.
 OS Magnaporthe grisea 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes incertae sedis; Magnaportheaceae; Magnaporthe.
 OX NCBI_TaxID=242507;
 RN [1]_TaxID=242507;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nussbaum C., Abebe A., Abouelleil A., Adekoya E.,
 RA Ait-zahra M., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Armbruster J., Bachantsang P., Baldwin J., Barry A.,
 RA Bayul T., Blithestreyn B., Bloom T., Blye J., Boguslavskiy L.,
 RA Borowsky M., Boukhgalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Cheshatsang Y., Citroen M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina A., Faro S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Gearin G., Gnerre S.,
 RA Gnilrke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hagos B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamvysseilis M., Karlsson E.,
 RA Kells C., Kieu A., Kisner P., Kodira C., Kulbokas E., Labutti K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis D., Lewis T.,
 RA Lindblad-toh K., Liu X., Lokytsang T., Lokytsang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,
 RA Manning J., Marabella R., Maru K., Matthews C., Maucelli E.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrim J., Meneus L.,
 RA Mesirov J., Mihalev A., Mihova T., Mikkelsen T., Mlenga V., Moru K.,
 RA Mozes J., Mulrain L., Munson G., Naylor J., Neues C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Osman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Retta R., Richardson S., Seaman C., Settipalli S., Sharpe T.,
 RA Rutnan M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougnez C.,
 RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stetson K., Stone S., Stone S., Stubbs M., Talamas J., Tchuang P.,
 RA Tensing P., Tesfaye S., Theodore J., Thoulutsang Y., Topham K.,
 RA Towey S., Tsanla T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whittaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee B., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Lander E.;
 RL "The genome sequence of Magnaporthe grisea";
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AACU01000121; EAA56157.1; -; Genomic DNA.
 DR InterPro; IPR000506; ACh_isomrdctse.
 DR InterPro; IPR009014; Transketo_C-like.
 DR Pfam; PF01450; ilvC; 1.
 DR TIGRFAMs; TIGR00465; ilvC; 1.
 KW Hypothetical protein.
 SQ SEQUENCE 400 AA; 44723 MW; 4C9B9B9E1495B6D75 CRC64;
 Query Match 89.2%; Score 1860; DB 2; Length 400;

OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.
OX NCBI_TaxID=237561;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Pederspiel N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000112; EAK94923.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE 400 AA; 44848 MW; ACD3162D05078D81 CRC64;

Query Match 73.8%; Score 1539.5; DB 2; Length 400;
Best Local Similarity 73.1%; Pred. No. 1e-100;
Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;
QY 1 MAARNCTKALRPLARQLATPAVORRTFVAASA-----VRASVAVKAAVAPARQOVRGKVT 56
DB 1 MSFRITSMRVARLATAKAT--LSKRTFSLANATTRYTAASSAAKAMTPTT--SIRGVKT 56
QY 57 MDPAGHKEEVRHADWPAEKLLDYFNKDTLALIGYSGQHGQGLNLDNGLNVIVGRKN 116
DB 57 INFGTTEVVRHADWPAEKLLDYFNKDTLALIGYSGQHGQGLNLDNGLNVIVGRK- 115
QY 117 GKSWDAIQDQWVPGKLVFDVDEAISRGTIVNNLLSDAAQSTWPHIKPQITKGKTLYS 176
DB 116 GSSWEAAVEDGWVPGENLFVDEAISRGTIIMDLLSDAAQSTWPHIKPQITKGKTLYS 175
QY 177 HGFSPVFKDLTKVEPTDVIIVAPKSGRTVRSIFREGGRINSFAYVDVTGKAEK 236
DB 176 HGFSPVFKDLTHVEPPSNDIVILAAPKSGRTVRSIFKEGRINSFAYVNDVTGKAEK 235
QY 237 AVALGVAVGSGYLTYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFN 296
DB 236 AIAATAIGSGYVYKTTTFRVNSDLYGERGCLMGHGMFLAQYEVLRENGHTPSEAFN 295
QY 297 ETVEEATQSLYPLIGAGHDMFDCSTTARRGAIDWTPKFDALKPVFNNDYSVKNGD 356
DB 296 ETVEEATQSLYPLIGKGYMDYDACSTTARRGALDWYPRFKDALKPVFEELYESYKNGS 355
QY 357 ERKRSLEYNSQDPRERYEAELDEIRNLEIWRAGK--RSLRPNQ 399
DB 356 ETKRSLEFNSRSDYKERLEEELQTIIRNMEIWRVGEVVKLRPNQ 400

RESULT 9
Q59XR8 CANAL PRELIMINARY; PRT; 400 AA.
AC Q59XR8;
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE Likely mitochondrial ketol-acid reductoisomerase.
GN Name=ILV5; ORFNames=CA019.88;
OS Candida albicans SC5314.
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; mitosporic Saccharomycetales; Candida.

OX NCBI_TaxID=237561;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RX PubMed=15123810; DOI=10.1073/pnas.0401648101;
RA Jones T., Pederspiel N.A., Chibana H., Dungan J., Kalman S., Magee P.T.,
RA Magee B.B., Newport G., Thorstenson Y.R., Agabian N., Magee P.T.,
RA Davis R.W., Scherer S.;
RT "The diploid genome sequence of Candida albicans.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:7329-7334 (2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=SC5314;
RA Dungan J., Kuo A., Newport G., Ian C.-Y., Iijima C., Adegbola O.,
RA Roberts J., Persson K., Donnelly S., Favoreto S., Tzung K.-W.,
RA Jones T., Scherer S., Agabian N.;
RT "Annotation of the Genome of Candida albicans.";
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AACQ01000106; EAK95225.1; -; Genomic_DNA.
KW Isomerase.
SQ SEQUENCE 400 AA; 44882 MW; FC79162D05078D8C CRC64;

Query Match 73.6%; Score 1535.5; DB 2; Length 400;
Best Local Similarity 72.8%; Pred. No. 1.9e-100;
Matches 295; Conservative 47; Mismatches 52; Indels 11; Gaps 5;
QY 1 MAARNCTKALRPLARQLATPAVORRTFVAASA-----VRASVAVKAAVAPARQOVRGKVT 56
DB 1 MSFRITSMRVARLATAKAT--LSKRTFSLANATTRYTAASSAAKAMTPTT--SIRGVKT 56
QY 57 MDPAGHKEEVRHADWPAEKLLDYFNKDTLALIGYSGQHGQGLNLDNGLNVIVGRKN 116
DB 57 INFGTTEVVRHADWPAEKLLDYFNKDTLALIGYSGQHGQGLNLDNGLNVIVGRK- 115
QY 117 GKSWDAIQDQWVPGKLVFDVDEAISRGTIVNNLLSDAAQSTWPHIKPQITKGKTLYS 176
DB 116 GSSWEAAVEDGWVPGENLFVDEAISRGTIIMDLLSDAAQSTWPHIKPQITKGKTLYS 175
QY 177 HGFSPVFKDLTKVEPTDVIIVAPKSGRTVRSIFREGGRINSFAYVDVTGKAEK 236
DB 176 HGFSPVFKDLTHVEPPSNDIVILAAPKSGRTVRSIFKEGRINSFAYVNDVTGKAEK 235
QY 237 AVALGVAVGSGYLTYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSEAFN 296
DB 236 AIAATAIGSGYVYKTTTFRVNSDLYGERGCLMGHGMFLAQYEVLRENGHTPSEAFN 295
QY 297 ETVEEATQSLYPLIGAGHDMFDCSTTARRGAIDWTPKFDALKPVFNNDYSVKNGD 356
DB 296 ETVEEATQSLYPLIGKGYMDYDACSTTARRGALDWYPRFKDALKPVFEELYESYKNGS 355
QY 357 ERKRSLEYNSQDPRERYEAELDEIRNLEIWRAGK--RSLRPNQ 399
DB 356 ETKRSLEFNSRSDYKERLEEELQTIIRNMEIWRVGEVVKLRPNQ 400

RESULT 10
Q6CY71 KLULA PRELIMINARY; PRT; 397 AA.
AC Q6CY71;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE Kluyveromyces lactis strain NRRL Y-1140 chromosome A of strain NRRL Y-1140 of Kluyveromyces lactis.
GN OrderedLocusNames=KLIA0A02673g;
OS Kluyveromyces lactis (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Kluyveromyces.
OX NCBI_TaxID=28985;
RN [1]

DR	GO:	GO:0005739;	C:mitochondrion; IDA.
DR	GO:	GO:0004455;	F:keto1-acid reductoisomerase activity; TAS.
DR	GO:	GO:0009082;	P:branched chain family amino acid biosynthesis; TAS.
DR	GO:	GO:0000002;	P:mitochondrial genome maintenance; IMP.
DR	InterPro:	IPR000506;	ACh_isomrdctse.
DR	Pfam:	PF01450;	ilvc; 1.
DR	TIGRFAMs:	TIGR00465;	ilvC; 1.
KW	Amino-acid biosynthesis;	Branched-chain amino acid biosynthesis;	
KW	Complete proteome;	Direct protein sequencing; Magnesium;	
KW	Mitochondrion; NADP;	Oxidoreductase; Transit peptide.	
FT	TRANSIT	1 47 Mitochondrion (Potential).	
FT	CHAIN	48 395 Ketol-acid reductoisomerase.	
FT	NP_BIND	84 93 NADP (Potential).	
FT	REGION	363 395 Hydrophilic.	
FT	ACT SITE	171 171 Potential.	
SQ	SEQUENCE	395 AA; 44368 MW; D76419A6AD68E85E CRC64;	
Query Match 72.3%; Score 1508.5; DB 1; Length 395;			
Best Local Similarity 73.6%; Pred. No. 1.6e-98;			
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;			
Qy	7	TKALRPRLARQLATPAVORRTFVAASAVRASVAKVAAPAAQOV-----RGVKTWDPFA 60	
Dd	4	TQAARLICNSRVITA--KRIF---ALATRAA----AYSRPAARFVKPMITTRGLKQINFG 54	
Qy	61	GKHEEVHERADWPAEKLDDYFKNDTLALIGYSOCHGQGNLRNGLNVI GVVRKGKSW 120	
Dd	55	GTVETVVERADWPREKLDDYFKNDTFALIGYSQGYQGGLNLRNGLNVIIGVRKDGASW 114	
Qy	121	EDAIQDQGWPGKNLFVDVEAISRTIYWNLLSDAAQSSETPHIKPOITKGTKLYFSHGFS 180	
Dd	115	KAATEDGWPGKNLFTVEDAIRKGSYWMNLLSDAAQSSETWPAIKPLLTCKGTYFSHGFS 174	
Qy	181	PVFKDLTKVEVPTDVIVLVAPKSGRTVSRLFREGGINSSFAVYQDVTGKAKEKAVAL 240	
Dd	175	PVFKDLTHVPPPKDLDILVAPKSGRTVSRLFKEGRGINSSAYVMNDVTGKAHEKAQAL 234	
Qy	241	GVAVGSGLYETTPKEVYSDLYGERCLMGHGMFLAOEVLRLERGHSPSEAFNETVE 300	
Dd	235	AVAIGSGYVQTTPEREVNSDLYGERCLMGHGMFLAQVDVURENGHSPSEAFNETVE 294	
Qy	301	EATQSLYLIGAHDMMFDACSTTARRGAIDMTPEKFDAIKPVFNNLXYSVKNKGDERKR 360	
Dd	295	EATQSLYLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVPQDIYSTKNGTETKR 354	
Qy	361	SLEVNSQPDYRERYEARLEIRNLWIWRACK--RSLRPENQ 399	
Dd	355	SLEFNSQPDYREKLKEKELDTIRNMEIWKGVEKVRKLRPENQ 395	
RESULT 12			
ID	Q02341_YEAST PRELIMINARY;	PRT;	395 AA.
AC	Q02341;		
DT	01-NOV-1996 (TrEMBLrel. 01, Created)		
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)		
DE	01-OCT-2003 (TrEMBLrel. 25, Last annotation update)		
DE	Acetohydroxy-acid isomeroreductase.		
GN	Names:ILV5; Synonyms:ILV5X;		
OS	Saccharomyces cerevisiae (Baker's yeast).		
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
OC	Saccharomycetales; Saccharomycetaceae; Saccharomycetes.		
NCBI_TaxID=4932;			
RN	[1]		
RP	NUCLEOTIDE SEQUENCE.		
RP	MEDLINE=95179732; PubMed=7874731; DOI=10.1007/BF00303925;		
RA	Xie Q., Jimenez A.;		
RT	"Cloning and molecular analysis of two different ILV5 genes from a		
RT	brewing strain of Saccharomyces cerevisiae.";		
RL	Curr. Genet. 26:398-402(1994).		
RL	EMBL; S77496; AAB33579.1; -; Genomic DNA.		
DR	HSSP; Q01292; IQMG.		
DR	Ensembl; YLR355C; Saccharomyces cerevisiae.		

Qy 2 AARNCTKALRPL-ARQLATPAVQRRTFVAAASAVRASVAVKAVAAPARQ-----Q 50

Db	6	SSRMAMKALRTMGSRRLATRSM-----SVWARTTAAPSMRPAPRTAPLMQ	51
Qy	51	VRGVKTMDFAGHKEEVEHERADWPAEKLLDYFKNDTTLALIGYQGHGQGLNRDGLNVI	110
Db	52	TRGMRVMDFAGTKENWERSDWPREKLVDYFKNDTTLAIIIGYQGHGQGLNARDQGLNVI	111
Qy	111	VGVRKNGKSWEDAIQDGWPGKNLFDVDEAISRTIIVMNLSDAAQSETWPHIKPOITKG	170
Db	112	VGVRKDGASWQIALEDGWVPGKTLFPVEEAIKKGSIIMNLLSDAAQSETWPKIAPLITKG	171
Qy	171	KTLYFSHGSPFVKDLTKVEVPTDVIDVLVAPKSGRTVRSLPREGRGINSSEFAVYQDVT	230
Db	172	KTLYFSHGSPFVKDLTKVHPKQDVVIDVLVAPKSGRTVRSLFKBGRGINSSEFAVYQDVT	231
Qy	231	GKAKEKAVAGVAVGSGYLITETFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGRHS	290
Db	232	GKAQEKAIGLAVAVGSGFYIQTTFKKEVISDLVGERGCLMGGINGLFLAQYQVLRERGRHS	291
Qy	291	PSAENETVEEATQSLYPLIGHGMWMDACSTTARRGAIDWTPFKDALKPVFNLYD	350
Db	292	PAEAFNETVEEATQSLYPLIGHGMWMDACSTTARRGAIDWTPFKDALKPVFNLYD	351
Qy	351	SVKNGDERKRSLEYNQPDYRERYEAELDEIRNLEIWRACK--RSLRPNQK	400
Db	352	NVNGENAKRSLEYNAPNYRELYDKLEELIRNLEIWKAGEVVRSLRPEHNK	403

RESULT 15

Q02340 YEAST

ID Q02340 YEAST PRELIMINARY; PRT; 395 AA.

AC Q02340;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)

DE Acetohydroxy-acid isomeroreductase.

GN Name=ILV5G;

OS Saccharomyces cerevisiae (Baker's yeast).

OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;

OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.

OX NCBI_TaxID=4932;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95179792; PubMed=7874731; DOI=10.1007/BF00309925;

RA Xie Q., Jimenez A.;

RT "Cloning and molecular analysis of two different ILV5 genes from a

RT brewing strain of Saccharomyces cerevisiae.";

RL Curr. Genet. 26:398-402(1994).

DR EMBL; S77495; AAB33578.1; -; Genomic_DNA.

DR HSSP; Q01292; 1QMG.

DR Ensembl; YLR355C; Saccharomyces cerevisiae.

DR GO; GO:0004455; F:keto1-acid reductoisomerase activity; IEA.

DR GO; GO:0009082; P:branched chain family amino acid biosynthesis; IEA.

DR InterPro; IPR000506; ACh_isomrdctse.

DR Pfam; PF01450; ILVc; 1.

DR TIGRFAMs; TIGR00465; ilvC; 1.

SQ SEQUENCE 395 AA; 44309 MW; 2F8BCD94FD7E2AEF CRC64;

Query Match

Best Local Similarity 70.9%; Score 1479.5; DB 2; Length 395;

Matches 288; Conservative 43; Mismatches 55; Indels 13; Gaps 4;

Qy	7	TKALRPLARQLATPAVQRTTFV----AAASAVPASVAVKAVAPARQQVGRVKTMDPAGH	62
Db	4	TOAARLICNSRVVTA--KRTFALATRAAAYSRPAARFVKPFWA-----TRGLKQINFGGT	56
Qy	63	KEEVHERADWPAEKLLDYFKNDTTLALIGYQGHGQGLNRDGLNVIIGVRKNGKSWED	122
Db	57	VEIVYERADWPREKLINLYFKDDTFALIGYQGHGQGLNRDGLNVIIGVRKDGASWKA	116
Qy	123	AIDQGWPGKNLFDVDEAISRTIIVMNLSDAAQSETWPHIKPOITKGKTLFSGHGFSPV	182
Db	117	AIEDGWVPGQNLFSVEDAIKKGNYVMNLSDAAQSETWPTIKPLLTGKTLFSGHGFSPV	176

Qy	183	FKDLTKVEVPTDVIDVLVAPKSGRTVRSLPREGRGINSSEFAVYQDVTGKAKEKAVAGV	242
Db	177	FKDLTHVEPPKDLVDVLVAPKSGRTVRSLFKBGRGINSSEFAVWMDVTGKAHEKAQALAV	236
Qy	243	AVGSGYLITETFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGRHSPEAFNETVEEA	302
Db	237	AIGSGYVYQTTFFEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEA	296
Qy	303	TQSLYPLIGHGMWMDACSTTARRGAIDWTPFKDALKPVFNLYDSVKNGDERKRS	362
Db	297	TQSLYPLIGKYGMDYMDACSTTARRGALDWYPIFKVALAPFVQDLYESTNGTETKRS	356
Qy	363	EYNQPDYRERYEAELDEIRNLEIWRACK--RSLRPNQK	399
Db	357	EFNSQPDYREKLEKELVTIRNMEIWKVGEVVKLRPENK	395

Search completed: March 22, 2006, 15:33:26

Job time : 126.313 secs

Search completed: March 22, 2006, 15:33:26
Job time : 126.313 secs

Qy	183	FKDLTKVEVPTDVIDVLVAPKSGRTVRSLPREGRGINSSEFAVYQDVTGKAKEKAVAGV	242
Db	177	FKDLTHVEPPKDLDDVLVAPKSGSGRTVRSLPFKEGGRGINSSEYAVMNDVTGKAHEKAQALAV	236
Qy	243	AVGSGYLYTETTFEKEVYSDLYGERGCLMGGIHGMFLAQYEVLRERGRHSSEAFNETVEEA	302
Db	237	AIGSGYVYQTTTTEREVNSDLYGERGCLMGGIHGMFLAQYDVLRENGHSPSEAFNETVEEA	296
Qy	303	TQSLYPLIGHGMWMDACSTTARRGAIDWTPFKDALKPVFNLYDSVKNGDERRKSL	362
Db	297	TQSLYPLIGHGMWMDACSTTARRGALDWYPIFKNALKPVFQDLVESTKNGTETKRSL	356
Qy	363	EYNSQPDYRERYEAELDEIRNLEIWRACK--RSLRPNQ	399
Db	357	EFNSQPDYREKLEKELVTIRNMEIWKVGEVKRLRPNK	395

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 114.954 Seconds
(without alignments)
1528.885 Million cell updates/sec

Title: US-10-797-248A-3
Perfect score: 2086
Sequence: 1 MAARNCTKALRPLARQLATP.....IRNLEIWRKRSILRPENQK 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A Geneseq 21.*
1: Geneseqp1980s.*
2: Geneseqp1990s.*
3: Geneseqp2000s.*
4: Geneseqp2001s.*
5: Geneseqp2002s.*
6: Geneseqp2003as.*
7: Geneseqp2003bs.*
8: Geneseqp2004s.*
9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2086	100.0	400	6	ABR64305
2	1860	89.2	400	6	ABR64306
3	1860	89.2	400	9	ADVI6807
4	1856	89.0	402	6	ABR64303
5	1658	79.5	403	9	ADVI6810
6	1633	78.3	396	6	ABJ26477
7	1633	78.3	508	6	ABJ26502
8	1604	76.9	388	6	ABJ25902
9	1604	76.9	500	6	ABJ25877
10	1539.5	73.8	400	4	AAU15089
11	1539.5	73.8	400	5	ABP73238
12	1508.5	72.3	395	6	ABR64304
13	1508.5	72.3	395	7	ADK64188
14	1423.5	68.2	409	7	ADB70124
15	1084.5	52.0	347	6	ABU20976
16	486	23.3	332	4	ABR96356
17	486	23.3	586	2	AAV26182
18	483	23.2	342	4	AAU01250
19	480.5	23.0	331	5	ABR48168
20	480.5	23.0	331	6	ABU32456
21	473	22.7	579	2	AAV26183
22	473	22.7	579	2	AAV26180
23	473	22.7	585	8	ADX93651
24	473	22.7	586	8	ADX88429

25	473	22.7	588	8	ADY07198
26	473	22.7	590	8	ADY07344
27	473	22.7	590	8	ADY07344
28	472.5	22.7	326	7	ADM26226
29	472.5	22.6	579	3	AAG35210
30	472	22.6	596	3	AAG35209
31	467	22.4	581	3	ADY61069
32	465	22.3	549	3	AAG26356
33	465	22.3	591	5	ABB92723
34	465	22.3	591	8	ADT55519
35	463	22.2	337	6	ABU24174
36	463	22.2	571	8	ADY04361
37	462	22.1	568	8	ADY07450
38	462	22.1	578	8	ADY92449
39	462	22.1	626	8	ADY07435
40	461.5	22.1	334	4	AAG81458
41	461.5	22.1	334	6	ABU42920
42	461.5	22.1	339	5	ABP39068
43	461.5	22.1	339	8	ADS07053
44	454.5	21.8	336	6	ABU18526
45	453.5	21.7	482	3	AAG26357

ALIGNMENTS

RESULT 1
ABR64305
ID ABR64305 standard; protein; 400 AA.
XX
AC ABR64305;
XX

DT 16-SEP-2003 (first entry)
XX

DE Acetohydroxyacid isomeroreductase.
XX

KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX

OS Neurospora crassa.
XX

PN FR2829363-A1.
XX

PD 14-MAR-2003.
XX

PF 10-SEP-2001; 2001PR-00011689.
XX

PR 10-SEP-2001; 2001PR-00011689.
XX

PA (AVET) AVENTIS CROPS SCIENCE SA.
XX

PI Dumas R; Lebrun MH, Zundel JL, Effantin G, Morin V;
XX

DR WPT; 2003-405775/39.
XX

PT Treatment of crops, useful for controlling fungi on, e.g. cereals, potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid isomeroreductase.
XX

PS Claim 2; Fig 1; 66pp; French.
XX

CC The present invention relates to a method for controlling fungal disease in crops by applying an inhibitor (I) of acetohydroxyacid isomeroreductase. (I) are used for curative or preventative treatment of a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or rape. The present sequence is an acetohydroxyacid isomeroreductase, used to illustrate the invention
XX

SQ Sequence 400 AA;
XX

Query Match 100.0%; Score 2086; DB 6; Length 400;
Best Local Similarity 100.0%; Pred. No. 2.1e-191;
Matches 400; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
DB 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
QY 61 GHKEEHERADWPAEKLDDYFKNDTLALIGYSGQGHGGLNLDNGLNVIIGVRKNGKSW 120
DB 61 GHKEEHERADWPAEKLDDYFKNDTLALIGYSGQGHGGLNLDNGLNVIIGVRKNGKSW 120
QY 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLFYFSGHS 180
DB 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLFYFSGHS 180
QY 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
DB 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
QY 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
DB 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
QY 301 EATQSLYPLIGAHGMDWDFACSTTARRGAIDWTPKFDALKEPVFNLYDSVKNGDERKR 360
DB 301 EATQSLYPLIGAHGMDWDFACSTTARRGAIDWTPKFDALKEPVFNLYDSVKNGDERKR 360
QY 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGKRSRLENQK 400
DB 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGKRSRLENQK 400

RESULT 2
ABR64306
ID ABR64306 standard; protein; 400 AA.
XX ABR64306;
AC ABR64306;
XX
DT 16-SEP-2003 (first entry)
XX
DE DE
DE Acetohydroxyacid isomeroreductas #2.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Magnaporthe grisea.
XX
PN FR2829363-A1.
XX
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET) AVENTIS CROPS SCIENCE SA.
XX
XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
PI
DR WPI; 2003-405775/39.
XX
DR N-PSDB; ACC80185, ACC80186.
XX

PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
PS Disclosure; Page 57-58; 66pp; French.
XX
CC The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase. (I) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 400 AA;

Query Match 89.2%; Score 1860; DB 6; Length 400;
Best Local Similarity 87.1%; Pred. No. 1.2e-169;
Matches 350; Conservative 34; Mismatches 14; Indels 4; Gaps 2;
QY 1 MAARNCTKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 60
DB 1 MSARGFSKALRPLARQLATPAVQRRTFVAAASAVRASVAVKAAVAPARQOVRGVKTMDF 58
QY 61 GHKEEHERADWPAEKLDDYFKNDTLALIGYSGQGHGGLNLDNGLNVIIGVRKNGKSW 120
DB 59 GHKEEHERADWPAEKLDDYFKNDTLALIGYSGQGHGGLNLDNGLNVIIGVRKNGKSW 118
QY 121 EDALQDQWPGKGLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLFYFSGHS 180
DB 119 KDAVQDQWPGKGLFEVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLFYFSGHS 178
QY 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSFLFREGGINSSFAVYQDVTGKAKEKAVAL 240
DB 179 PVFKDLTKVEVPTDVIDVILCAPKSGRTVRSFLFREGGINSSFAVYQDVTGAEAEKAI 238
QY 241 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 300
DB 239 GVAVGSGLYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERGHSPSEAFNETVE 298
QY 301 EATQSLYPLIGAHGMDWDFACSTTARRGAIDWTPKFDALKEPVFNLYDSVKNGDERKR 360
DB 299 EATQSLYPLIGAHGMDWDFACSTTARRGAIDWTPKFDALKEPVFNLYDSVKNGSETQR 358
QY 361 SLEYNQPDYRERYEAELDEIRNLEIWRAGK--RSRLENQK 400
DB 359 SLDYNSQPDYREKYEAEEMEIRNLEIWRAGKAVRSRLENQK 400
RESULT 3
ADV16807
ID ADV16807 standard; protein; 400 AA.
XX ADV16807;
AC ADV16807;
XX
DT 24-FEB-2005 (first entry)
XX
DE M grisea ketol-acid reductoisomerase ILV5 seqid 6.
XX
KW substrate inhibition; antibiotic; gene disruption;
KW ketol-acid reductoisomerase; ILV5, enzyme.
XX
OS Magnaporthe grisea.
XX
PN WO2004104176-A2.
XX
PD 02-DEC-2004.
XX
PF 17-MAY-2004; 2004WO-US015404.
XX
PR 15-MAY-2003; 2003US-0470947P.
PR 19-MAY-2003; 2003US-0471615P.
PR 21-MAY-2003; 2003US-0472242P.
XX
PA (PARA-) PARADIGM GENETICS INC.
XX
PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
PI Montenegro-Chamorro MV, Darveaux BA, Frank SA, Heiniger RW;
PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
XX
DR WPI; 2005-021202/02.
DR N-PSDB; ADV16805, ADV16806.
XX
PT Identifying a test compound as a candidate for an antibiotic comprises
PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
PT with a test compound.
XX
PS Claim 48; SEQ ID NO 6; 179pp; English.

XX The invention describes a method of identifying a test compound as a
 CC candidate for an antibiotic comprising contacting ornithine
 CC carbamoyltransferase (Ocrase) or ketol-acid reductoisomerase polypeptide,
 CC or fungal pathogenicity-conferring gene with a test compound. The method
 CC comprises: contacting Ocrase polypeptide, ketol-acid reductoisomerase
 CC polypeptide, or fungal pathogenicity-conferring gene with a test compound
 CC ; and detecting the presence or absence of binding between the test
 CC compound and the polypeptide or gene, where binding indicates that the
 CC test compound is a candidate for an antibiotic. Also described are: an
 CC isolated nucleic acid comprising a nucleotide sequence encoding a
 CC polypeptide having at least 50% sequence identity to, or having at least
 CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated
 CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
 XX
 SQ Sequence 400 AA;

Query Match 89.2%; Score 1860; DB 9; Length 400;
 Best Local Similarity 87.1%; Pred. No. 1.2e-169;
 Matches 350; Conservative 34; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MAARNCTKALRPLARQLATPAVQRRTFAAASAVRASVAVKAAAPARQVGVKTMDF 60
 Db 1 MSARGFSKALRPMARQLATPAVQRRTFAAASAVRASVAVKAAAPARQVGVKTMDF 58
 Qy 61 GHKEEYHERADWPAEKLLDYFKNDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 120
 Db 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 118
 Qy 121 EDATQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 180
 Db 119 KDAVQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 178
 Qy 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLPREGGINSSFAVYQDVTGKAKEKAV 240
 Db 179 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLPREGGINSSFAVYQDVTGKAKEKAV 238
 Qy 241 GVAVGSGLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 300
 Db 239 GVAIGSGLYKTTTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 Qy 301 EATQSLYPLIGAHGMDWMFACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 360
 Db 299 EATQSLYPLIGAHGMDWMFACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 358
 Qy 361 SLEYNQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
 Db 359 SLDYNSQPDYRERYEAELEIRNLEIWRAGKAVRSRLENQK 400

RESULT 4

ABR64303
 ID ABR64303 standard; protein; 402 AA.

XX ABR64303;

XX 16-SEP-2003 (first entry)

XX Acetohydroxyacid isomeroreductase #1.

DE Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.

XX Magnaporthe grisea.

XX FR2829363-A1.

XX 14-MAR-2003.

XX 10-SEP-2001; 2001FR-00011689.

XX 10-SEP-2001; 2001FR-00011689.

XX (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;

XX WPI; 2003-405775/39.

XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
 PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 PT isomeroreductase.

XX Claim 2; Fig 1; 66pp; French.

XX The present invention relates to a method for controlling fungal disease
 CC in crops by applying an inhibitor (I) of acetohydroxyacid
 CC isomeroreductase (IR) are used for curative or preventative treatment of
 CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
 CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
 CC to illustrate the invention

XX Sequence 402 AA;

Query Match 89.0%; Score 1856; DB 6; Length 402;
 Best Local Similarity 86.8%; Pred. No. 2.8e-169;
 Matches 349; Conservative 35; Mismatches 14; Indels 4; Gaps 2;

Qy 1 MAARNCTKALRPLARQLATPAVQRRTFAAASAVRASVAVKAAAPARQVGVKTMDF 60
 Db 1 MSARGFSKALRPMARQLATPAVQRRTFAAASAVRASVAVKAAAPARQVGVKTMDF 58
 Qy 61 GHKEEYHERADWPAEKLLDYFKNDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 120
 Db 59 GHKEQWVERADWPKEKLEFYKDDTLALIGYSGQGGQGLNLDNGLNVIIGVRKNGKSW 118
 Qy 121 EDATQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 180
 Db 119 KDAVQDQWVPGKGLFDVDEAISRGITVIMNLLSDAAQSETWPHIKPQITKGTLYFSHGFS 178
 Qy 181 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLPREGGINSSFAVYQDVTGKAKEKAV 240
 Db 179 PVFKDLTKVEVPTDVIDVILVAPKSGRTVRSLPREGGINSSFAVYQDVTGKAKEKAV 238
 Qy 241 GVAVGSGLYETTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 300
 Db 239 GVAIGSGLYKTTTFEKEVYSDLYGERGCLMGGHGMFLAQYEVLRERGHSPSEAFNETVE 298
 Qy 301 EATQSLYPLIGAHGMDWMFACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 360
 Db 299 EATQSLYPLIGAHGMDWMFACSTTARRGAIDWTPKFKDALKPFVFNLYDSVKNGBERKR 358
 Qy 361 SLEYNQPDYRERYEAELEIRNLEIWRAGK--RSLRPENQK 400
 Db 359 SLDYNSQPDYRERYEAELEIRNLEIWRAGKAVRSRLENQK 400

RESULT 5

ADVL6810
 ID ADVL6810 standard; protein; 403 AA.

XX ADVL6810;

XX 24-FEB-2005 (first entry)

XX M graminicola ketol-acid reductoisomerase KAR1 seqid 9.

XX substrate inhibition; antibiotic; gene disruption;

XX ketol-acid reductoisomerase; KAR1; enzyme.

XX Mycosphaerella graminicola.

XX WO2004104176-A2.

XX PD 02-DEC-2004.

XX PF 17-MAY-2004; 2004WO-US015404.

XX PR 15-MAY-2003; 2003US-0470947P.

XX PR 19-MAY-2003; 2003US-0471615P.

XX PR 21-MAY-2003; 2003US-0472242P.

XX PA (PARA-) PARADIGM GENETICS INC.

XX PI Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;

XX PI Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;

XX PI Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;

XX DR WPI: 2005-021202/02.

XX DR N-PSDB; ADV16802, ADV16808, ADV16809.

XX PT Identifying a test compound as a candidate for an antibiotic comprises

XX PT contacting ornithine carbamoyltransferase (OCTase) or ketol-acid

XX PT reductoisomerase polypeptide, or fungal pathogenicity-conferring gene

XX PT with a test compound.

XX PS Claim 50; SEQ ID NO 9; 179pp; English.

XX CC The invention describes a method of identifying a test compound as a

XX CC candidate for an antibiotic comprising contacting ornithine

XX CC carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,

XX CC or fungal pathogenicity-conferring gene with a test compound. The method

XX CC comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase

XX CC polypeptide, or fungal pathogenicity-conferring gene with a test compound

XX CC ; and detecting the presence or absence of binding between the test

XX CC compound and the polypeptide or gene, where binding indicates that the

XX CC test compound is a candidate for an antibiotic. Also described are: an

XX CC isolated nucleic acid comprising a nucleotide sequence encoding a

XX CC polypeptide having at least 50% sequence identity to, or having at least

XX CC 10% of the activity of, 400, 403 or 469 amino acids; and an isolated

XX CC polypeptide consisting essentially of the amino acid sequence of 400, 403

XX CC or 469 amino acids. The methods are useful for identifying inhibitors of

XX CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal

XX CC pathogenicity-conferring gene as antibiotics. This is the amino acid

XX CC sequence of *Mycosphaerella graminicola* ketol-acid reductoisomerase KAR1.

XX SQ Sequence 403 AA;

Query Match 79.5%; Score 1658; DB 9; Length 403;

Best Local Similarity 78.4%; Pred. No. 3.2e-150;

Matches 315; Conservative 40; Mismatches 43; Indels 4; Gaps 2;

QY 1 MAARNCTKALRPLARQLATPAVORRTFVAAGAASAVRASV--AVKAAVAPARQQVRGKTKWD 58

DB 1 MASKNATRALRASLRQLKAPQVQORSFVAANASRSLVPAQAVTSFVQVVRGAKTVVD 60

QY 59 FAGHKEEVEHADWPAAEKLLDYPKNDTLALIGYSGHQGLNRDNLNVLVIGVRKNGK 118

DB 61 FAGDKKVFERDDWPREKLLFYKNDTLALIGYSGHQGLNRDNLNVLVIGVRKNGA 120

QY 119 SNEDALQDCWVGPKNLFVDVEALSRTIWNLLSDAAQSETWPHIKPQTKGKTLFSGH 178

DB 121 SWKEAEGDGVGKGNLFDDTAIGKGTIIWNLLSDAAQSETWPHIKPMLTKGKTLFSGH 180

QY 179 FSPVFVKDLTKVEVPTDVIDVLVAPKSGRTVRSRPREGRGINSFVAVYQDVTGKAKAV 238

DB 181 FSPVFVKDLTKVEVPTDVIDVLVAPKSGRTVRSRPREGRGINSFVAVYQDVTGKAKAV 240

QY 239 ALGVAVSGYLYETTFKEVYSDLYGERCLMGHGMFLAQYEVLRERGHSPSEAFNET 298

DB 241 ALGVAVSGYMYKTTTKEVYSDLYGERCLMGHGMFLAQYEVLRERGHSPSEAFNET 300

QY 299 VEATOSLYPLTGAHGMDFACSTTARRGAIDWTPEKFDALKPVFNLLYSVKNQDGR 358

DB 301 VEATOSLYPLTGNKGMDFYACSTTARRGAIDWSKRFKTKLPVFEELYDSVTKGT 360

QY 359 KRSLEYNQPDYRYERYAELEIRNLEIWRACK--RSLRPEN 398

DB 361 QRTMEYAGKDYREAFKEMEIRNLEIWRACKAVRSLRPEN 402

RESULT 6

ABJ26477

ID ABJ26477 standard; protein; 396 AA.

XX AC ABJ26477;

XX DT 16-APR-2003 (first entry)

XX DE Aspergillus fumigatus essential gene protein #1135.

XX KW Fungicide; cytostatic; essential gene; *Aspergillus fumigatus*; infection;

XX KW cancer; contamination; biofilm; antibody; immune response.

XX OS *Aspergillus fumigatus*.

XX PN WO200286090-A2.

XX PD 31-OCT-2002.

XX PF 23-APR-2002; 2002WO-US013142.

XX PR 23-APR-2001; 2001US-0285697P.

XX PR 27-APR-2001; 2001US-0287066P.

XX PR 05-JUN-2001; 2001US-0295890P.

XX PR 09-JUL-2001; 2001US-0303899P.

XX PR 31-AUG-2001; 2001US-0316362P.

XX PA (ELIT-) ELITRA PHARM INC.

XX PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;

XX WPI: 2003-093124/08.

XX PT New purified or isolated nucleic acids of essential genes of *Aspergillus*

XX PT *fumigatus*, useful for treating or preventing infections by *A. fumigatus*,

XX PT or for treating a non-infectious disease in a subject e.g. cancer.

XX PS Disclosure; Page; 175pp; English.

XX CC The invention relates to novel purified or isolated nucleic acids of

XX CC essential genes of *Aspergillus fumigatus*. The isolated nucleic acids of

XX CC the invention are used to treat or prevent infections by a pathogenic

XX CC organism such as *A. fumigatus*, to treat a non-infectious disease in a

XX CC subject (e.g. cancer), to prevent or contain contamination of an object

XX CC by *A. fumigatus*, or to prevent or inhibit formation on a surface of a

XX CC biofilm comprising *A. fumigatus*. The polynucleotides are useful for

XX CC expressing recombinant protein for characterisation, screening or

XX CC therapeutic use, as markers for host tissues in which the pathogenic

XX CC organisms invade or reside, for comparing with the DNA sequence of *A.*

XX CC *fumigatus* to identify duplicated genes or paralogues having the same or

XX CC similar biochemical activity and/or function, for comparing with DNA

XX CC sequences of other related or distant pathogenic organisms to identify

XX CC potential orthologous essential or virulence genes, for selecting and

XX CC making oligomers for attachment to a nucleic acid array for examination

XX CC of expression patterns, for raising anti-protein antibodies, as an

XX CC antigen to raise anti-DNA antibodies or to elicit another immune

XX CC response, and for identifying polynucleotides encoding the other protein

XX CC with which binding occurs or to identify inhibitors of the binding

XX CC interaction. The polypeptides may be used to raise antibodies or to

XX CC elicit immune response, as a reagent in assays designed to quantitatively

XX CC determine levels of the protein in biological fluids, as a marker for

XX CC host tissues in which pathogenic organism invade or reside, and to

XX CC isolate correlative receptors or ligands in the case of virulence

XX CC factors. This sequence represents a protein of one of the essential genes

XX CC of *Aspergillus fumigatus* of the invention

XX SQ Sequence 396 AA;

Query Match 78.3%; Score 1633; DB 6; Length 396;
 Best Local Similarity 78.6%; Pred. No. 7.9e-148;
 Matches 319; Conservative 35; Mismatches 36; Indels 16; Gaps 6;

QY 1 MAARNCTKALRPLARQATPAVQRRTFVAAA-----SAVRASVAVKAAVAPARQOVRGKVT 56
 DB 1 MASRGLPRALR-LAR-VAAP-----RTVISALPRPALAKAATRAASTAP-----VRGKVT 50

QY 57 MDPAGHKEEVEHERADWPAEKLLDYFNKNDTLALIGYSGHGGQGLNLDNGNLNIVGVKRN 116
 DB 51 IAFADSKETVYERADWPPEKLEQYFKNDTLALIGYSGHGGQGLNLDNGNLNIVGVKRD 110

QY 117 GKSMEDATODGWPGKNLFDVDEALSRGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 176
 DB 111 GASWKAIDQGWIPGKNLFDLTAQVQGTIVMNLSDAAQSETWPTKPLITKGTLYFS 170

QY 177 HGFSPVFKELTKVVEPTDVIDVILVAPKSGRTVRSLEFREGGINSSFAVYQDVGTGKAKEK 236
 DB 171 HGFSPVFKELTKVDVPKDVILVAPKSGRTVTLFREGGINSSFAVYQDVGTGKAKEK 230

QY 237 AVALGVAVSGSYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSFAFN 296
 DB 231 AIAMGVAVSGSYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSFAFN 290

QY 297 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWTPKPKDALKPVFNLYDSVKNGD 356
 DB 291 ETVEEATOSLYPLIGAGMDWMDYACSTTARRGAIDWSSRFKDTLPKIPFNELYDSVRDGT 350

QY 357 ERKRSLEYNQDYPYRYEAELEIRNLEIWRAGKR--SLRPNQK 400
 DB 351 ETKRSLEYNQDKYREYKEMQDIRDLLEIWRAGKAVGSLRPNQK 396

RESULT 7
 ID ABJ26502 standard; protein; 508 AA.
 AC ABJ26502;
 XX
 XX
 DT 16-APR-2003 (first entry)
 XX
 XX Aspergillus fumigatus essential gene protein #1160.
 DE
 XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KW cancer; contamination; biofilm; antibody; immune response.
 XX
 OS Aspergillus fumigatus.
 XX
 XX WO200286090-A2.
 XX
 XX 31-OCT-2002.
 XX
 XX 23-APR-2002; 2002WO-US013142.
 XX
 XX 23-APR-2001; 2001US-0285697P.
 XX
 XX 27-APR-2001; 2001US-0287066P.
 XX
 XX 05-JUN-2001; 2001US-0295890P.
 XX
 XX 09-JUL-2001; 2001US-0303899P.
 XX
 XX 31-AUG-2001; 2001US-0316362P.
 XX
 XX (ELIT-) ELITPA PHARM INC.
 XX
 XX Jiang B, Tishkoff D, Zamudio C, Broshkin AM, Hu W, Lemieux SM;
 XX WPI; 2003-093124/08.
 XX
 XX New purified or isolated nucleic acids of essential genes of Aspergillus
 PT fumigatus, useful for treating or preventing infections by A. fumigatus,
 PT or for treating a non-infectious disease in a subject e.g. cancer.
 XX
 XX Disclosure; Page: 175pp; English.
 PS
 XX The invention relates to novel purified or isolated nucleic acids of

essential genes of Aspergillus fumigatus. The isolated nucleic acids of
 the invention are used to treat or prevent infections by a pathogenic
 organism such as A. fumigatus, to treat a non-infectious disease in a
 subject (e.g. cancer), to prevent or contain contamination of an object
 by A. fumigatus, or to prevent or inhibit formation on a surface of a
 biofilm comprising A. fumigatus. The polynucleotides are useful for
 expressing recombinant protein for characterization, screening or
 therapeutic use, as markers for host tissues in which the pathogenic
 organisms invade or reside, for comparing with the DNA sequence of A.
 fumigatus to identify duplicated genes or paralogues having the same or
 similar biochemical activity and/or function, for comparing with DNA
 sequences of other related or distant pathogenic organisms to identify
 potential orthologous essential or virulence genes, for selecting and
 making oligomers for attachment to a nucleic acid array for examination
 of expression patterns, for raising anti-protein antibodies, as an
 antigen to raise anti-DNA antibodies or to elicit another immune
 response, and for identifying polynucleotides encoding the other protein
 with which binding occurs or to identify inhibitors of the binding
 interaction. The polypeptides may be used to raise antibodies or to
 elicit immune response, as a reagent in assays designed to quantitatively
 determine levels of the protein in biological fluids, as a marker for
 host tissues in which pathogenic organism invade or reside, and to
 isolate correlative receptors or ligands in the case or virulence
 factors. This sequence represents a protein of one of the essential genes
 of Aspergillus fumigatus of the invention

XX
 SQ Sequence 508 AA;

Query Match 78.3%; Score 1633; DB 6; Length 508;
 Best Local Similarity 78.6%; Pred. No. 1.2e-147;
 Matches 319; Conservative 35; Mismatches 36; Indels 16; Gaps 6;

QY 1 MAARNCTKALRPLARQATPAVQRRTFVAAA-----SAVRASVAVKAAVAPARQOVRGKVT 56
 DB 113 MASRGLPRALR-LAR-VAAP-----RTVISALPRPALAKAATRAASTAP-----VRGKVT 162

QY 57 MDPAGHKEEVEHERADWPAEKLLDYFNKNDTLALIGYSGHGGQGLNLDNGNLNIVGVKRN 116
 DB 163 IAFADSKETVYERADWPPEKLEQYFKNDTLALIGYSGHGGQGLNLDNGNLNIVGVKRD 222

QY 117 GKSMEDATODGWPGKNLFDVDEALSRGTIVMNLSDAAQSETWPHIKPOITKGTLYFS 176
 DB 223 GASWKAIDQGWIPGKNLFDLTAQVQGTIVMNLSDAAQSETWPTKPLITKGTLYFS 282

QY 177 HGFSPVFKELTKVVEPTDVIDVILVAPKSGRTVRSLEFREGGINSSFAVYQDVGTGKAKEK 236
 DB 283 HGFSPVFKELTKVDVPKDVILVAPKSGRTVTLFREGGINSSFAVYQDVGTGKAKEK 342

QY 237 AVALGVAVSGSYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSFAFN 296
 DB 343 AIAMGVAVSGSYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERHSPSFAFN 402

QY 297 ETVEEATOSLYPLIGAGMDWMDACSTTARRGAIDWTPKPKDALKPVFNLYDSVKNGD 356
 DB 403 ETVEEATOSLYPLIGAGMDWMDYACSTTARRGAIDWSSRFKDTLPKIPFNELYDSVRDGT 462

QY 357 ERKRSLEYNQDYPYRYEAELEIRNLEIWRAGKR--SLRPNQK 400
 DB 463 ETKRSLEYNQDKYREYKEMQDIRDLLEIWRAGKAVGSLRPNQK 508

RESULT 8
 ID ABJ25902 standard; protein; 388 AA.
 XX
 XX ABJ25902;
 AC
 XX
 XX 16-APR-2003 (first entry)
 DT
 XX Aspergillus fumigatus essential gene protein #560.
 DE
 XX Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
 KW cancer; contamination; biofilm; antibody; immune response.

CC with which binding occurs or to identify inhibitors of the binding
 CC interaction. The polypeptides may be used to raise antibodies or to
 CC elicit immune response, as a reagent in assays designed to quantitatively
 CC determine levels of the protein in biological fluids, as a marker for
 CC host tissues in which pathogenic organism invade or reside, and to
 CC isolate correlative receptors or ligands in the case of virulence
 CC factors. This sequence represents a protein of one of the essential genes
 CC of *Aspergillus fumigatus* of the invention
 XX
 SQ Sequence 500 AA;
 Query Match 76.9%; Score 1604; DB 6; Length 500;
 Best Local Similarity 78.7%; Pred. No. 6.9e-145;
 Matches 311; Conservative 35; Mismatches 35; Indels 14; Gaps 5;
 QY 1 MAARNCTKALRPLARQIATPAVQRRTFVAASA-----SAVRASVAVKAVAPARQOVRGVT 56
 DB 113 MASRGLPALR-LAR-VAAP-----RTVISAALPRPALAKAATRVAASTAP-----VRGVT 162
 QY 57 MDPAGHKEEVEHRAADWPAEKLLDYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVKN 116
 DB 163 IAFADSKETVYERADWPKEKLOEYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVKN 222
 QY 117 GKSWEADAIQDQGWPGKNLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLIFS 176
 DB 223 GASWEADAIQDQGWPGKNLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLIFS 282
 QY 177 HGFSVPFKDLTKVEPTDNDVILVAPKSGRTVRSLEFRGGINSSPFAVYQDVTGKAKEK 236
 DB 283 HGFSVPFKDLTKVDVDPKDVILVAPKSGRTVRSLEFRGGINSSPFAVYQDVTGKAKEK 342
 QY 237 AVALGVAVGSGYLTYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERHSPSEAFN 296
 DB 343 AIAMGVAVGSGYLTYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERHSPSEAFN 402
 QY 297 ETVEEATQSLYPLIGAHGMDWDFDACSCTTARRGAIDWTPKFDALKPVENNLYDSVKNQD 356
 DB 403 ETVEEATQSLYPLIGAHGMDWDFDACSCTTARRGAIDWTPKFDALKPVENNLYDSVKNQD 462
 QY 357 ERKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK 391
 DB 463 ETKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK 497
 RESULT 10
 AAU15089
 ID AAU15089 standard; protein; 400 AA.
 XX
 AC AAU15089;
 XX
 XX 04-DEC-2001 (first entry)
 XX
 XX Protein encoded by *C. albicans* essential gene *CaYLR355C* (ILV5).
 DE
 XX Gene identification; essential gene; GRACE; pathogenic fungus;
 KW gene replacement and conditional expression; fungal infection.
 XX
 XX Candida albicans.
 OS
 XX WO200160975-A2.
 XX
 XX 23-AUG-2001.
 XX
 XX 20-FEB-2001; 2001WO-US005551.
 XX
 XX 18-FEB-2000; 2000US-0183534P.
 XX
 XX (ELIT-) ELITRA PHARM INC.
 PA
 XX Roemer T, Jiang B, Boone C, Bussey H;
 XX
 XX WPI; 2001-489080/53.
 XX
 XX N-PSDB; AAS23417.
 DR

XX Identifying genes essential to fungal metabolisms and identifying
 PT potential therapeutic agents that target these genes.
 XX
 PS Claim 43; Page 222-223; 324pp; English.
 XX
 CC The present invention relates to novel methods for constructing fungal
 CC strains useful for identification and validation of gene products as
 CC targets for therapeutic agents, for creating a collection of identified
 CC essential genes, and screening assays for the discovery of new drugs. The
 CC invention provides the GRACE (gene replacement and conditional
 CC expression) method for the construction of mutant organisms referred to
 CC as GRACE strains of the organism. The invention can be applied to any
 CC organism, particularly a pathogenic fungus e.g. *Candida albicans*,
 CC *Aspergillus fumigatus* and *Cryptococcus neoformans*. The methods are useful
 CC to identify agents that may be used in the treatment of fungal
 CC infections. AAU15053-AAU15113 represent proteins encoded by *C. albicans*
 CC essential genes
 XX
 SQ Sequence 400 AA;
 Query Match 73.8%; Score 1539.5; DB 4; Length 400;
 Best Local Similarity 73.1%; Pred. No. 7.9e-139;
 Matches 296; Conservative 47; Mismatches 51; Indels 11; Gaps 5;
 QY 1 MAARNCTKALRPLARQIATPAVQRRTFVAASA-----VRASVAVKAVAPARQOVRGVT 56
 DB 1 MSPRTTSMRMARLATAKAT--LSKRTFSLANATTRYTAASSAAKAMTPTT--SIRGVT 56
 QY 57 MDPAGHKEEVEHRAADWPAEKLLDYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVKN 116
 DB 57 INFEGTTEVVHRAADWPAEKLLDYFNKDTLALIGYSGHGGQGLNLRDGLNIVGVKN 115
 QY 117 GKSWEADAIQDQGWPGKNLFDVDEAISRGTTVMNLLSDAAQSETWPHIKPOITKGKTLIFS 176
 DB 116 GSWEEAAVEDGWPGENLFEVDEAISRGTTIMDLSDDAAQSETWPHIKPOITKGKTLIFS 175
 QY 177 HGFSVPFKDLTKVEPTDNDVILVAPKSGRTVRSLEFRGGINSSPFAVYQDVTGKAKEK 236
 DB 176 HGFSVPFKDLTKVEPTDNDVILVAPKSGRTVRSLEFRGGINSSPFAVYQDVTGKAKEK 235
 QY 237 AVALGVAVGSGYLTYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERHSPSEAFN 296
 DB 236 AIAMGVAVGSGYLTYETTFEKEVSDLYGERGCLMGGIHGMFLAQYEVLRERHSPSEAFN 295
 QY 297 ETVEEATQSLYPLIGAHGMDWDFDACSCTTARRGAIDWTPKFDALKPVENNLYDSVKNQD 356
 DB 296 ETVEEATQSLYPLIGAHGMDWDFDACSCTTARRGAIDWTPKFDALKPVENNLYDSVKNQD 355
 QY 357 ERKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK--RSLRPENQ 399
 DB 356 ETKRSLEYNQPDYRERYEAELDEIRNLEIWRAGK 400
 RESULT 11
 ABP73238
 ID ABP73238 standard; protein; 400 AA.
 XX
 AC ABP73238;
 XX
 XX 30-JAN-2003 (first entry)
 XX
 XX Candida albicans essential protein SEQ ID NO 7075.
 DE
 XX Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
 KW signal transduction; DNA replication; cell division; growth;
 XX proliferation; Candida albicans; fungicide; antifungal.
 XX
 XX Candida albicans.
 OS
 XX WO200253728-A2.
 XX
 XX 11-JUL-2002.
 PD

CC the printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pat_sequences.

PT for homologous nucleic acids required for cellular proliferation to
PT isolate candidate molecules for rational drug discovery programs.

XX SQ Sequence 409 AA;

XX Claim 25; SEQ ID NO 48900; 1766pp; English.

Query Match 68.2%; Score 1423.5; DB 7; Length 409;
Best Local Similarity 70.2%; Pred. No. 1.2e-127;
Matches 278; Conservative 47; Mismatches 62; Indels 9; Gaps 3;

CC The invention relates to an isolated nucleic acid comprising any one of
CC the 6213 antisense sequences given in the specification where expression
CC of the nucleic acid inhibits proliferation of a cell. Also included are:
CC (1) a vector comprising a promoter operably linked to the nucleic acid
CC encoding a polypeptide whose expression is inhibited by the antisense
CC nucleic acid; (2) a host cell containing the vector; (3) an isolated
CC polypeptide or its fragment whose expression is inhibited by the
CC antisense nucleic acid; (4) an antibody capable of specifically binding
CC the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular
CC proliferation or the activity of a gene in an operon required for
CC proliferation; (7) identifying a compound that influences the activity of
CC the gene product or that has an activity against a biological pathway
CC required for proliferation, or that inhibits cellular proliferation; (8)
CC identifying a gene required for cellular proliferation or the biological
CC pathway in which a proliferation-required gene or its gene product lies
CC or a gene on which the test compound that inhibits proliferation of an
CC organism acts; (9) manufacturing an antibiotic; (10) profiling a
CC compound's activity; (11) a culture comprising strains in which the gene
CC product is overexpressed or underexpressed; (12) determining the extent
CC to which each of the strains is present in a culture or collection of
CC strains; or (13) identifying the target of a compound that inhibits the
CC proliferation of an organism. The antisense nucleic acids are useful for
CC identifying proteins or screening for homologous nucleic acids required
CC for cellular proliferation to isolate candidate molecules for rational
CC drug discovery programs, or for screening homologous nucleic acids
CC required for proliferation in cells other than *S. aureus*, *S. typhimurium*,
CC *K. pneumoniae* or *P. aeruginosa*. The present sequence is encoded by one of
CC the target prokaryotic essential genes. Note: The sequence data for this
CC patent did not form part of the printed specification, but was obtained
CC in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pat_sequences

XX SQ Sequence 347 AA;

XX Query Match 52.0%; Score 1084.5; DB 6; Length 347;
XX Best Local Similarity 59.9%; Pred. No. 3.8e-95;
XX Matches 206; Conservative 51; Mismatches 84; Indels 3; Gaps 2;

QY 3 ARNCTKALRPLARQLATPAVQRRTF-VAAASAVRASVAVKAAAPARQQVGRVKTMDFAG 61

QY 57 MDPAGHKEVHERADWPAEKLLDYPKNDTLALIGYSGHGGQGLNLRDNLGNVIVGRKN 116

Db 4 SRASNALKQALKSTASQVARSYSLLSGAAPRAAMATLGA-----TRGIKTLDFAG 57

Db 4 LNFGGVTVNVVTRREBFPLEKAREVLKNETIIVIGYGVQVQGSQSLNLRDNGFNIVGQRP- 62

QY 62 HKEVEHERADWPAEKLLDYPKNDTLALIGYSGHGGQGLNLRDNLGNVIVGRKNGKSW 121

QY 117 GKSWEIDAQDGVPGKVLFDVDEAISRGTIVMNLSDAAQSETWPHIKPQITKGTLYFS 176

Db 58 TKEVVYERADWPLDKLDQVFPKNDTLAMIGYSGHGGQSLNARDNLGLKVIIVGRKGSWK 117

Db 63 GRTYKAVADGWVPGETLFGIEEACEKGTIIMCLSDAAVMSVWPTIKPVLTAGKALYFS 122

QY 122 DAIQDGVPGKVLFDVDEAISRGTIVMNLSDAAQSETWPHIKPQITKGTLYFSHGFS 181

QY 177 HGFSVPVKDLTKVEVPTDVIDLVAPKSGSRVTSIFREGRGINSFVAYQDVDTGKAKEK 236

Db 118 QAQEDGVPGETLFDPEALKNGTIIIMNLSDAAQSQTNWNEIAPLITKGTLYFAHGF 177

Db 123 HGFAITWSDRTGVPQKIDIVMVPKSGTSLRTWFLREGRLNSYAIYQDATGEAMER 182

QY 182 VFKDLTKVEVPTDVIDLVAPKSGSRVTSIFREGRGINSFVAYQDVDTGKAKEKAVAG 241

QY 237 AVAGLVAGSGYLTYETTFEKEVYSDLYGBERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 296

Db 178 VYKEDTHVIPPDKVDVILVAPKSGRTVTLFLEGRGINSSIAVYQDVDTGHAKEKAVAG 237

Db 242 VAVSGYLTYETTFEKEVYSDLYGBERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 301

QY 242 VAVSGYLTYETTFEKEVYSDLYGBERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 301

QY 362 LEYNSQPDYRERYAELEIRNLEIWRAGK--RSLR 395

Db 238 IAVSGYLTYETTFEKEVYSDLYGBERGCLMGGIHGMFLAQYEVLRERGHSPSEAFN 297

Db 357 ERKRSLEYNQPDYRERYAELEIRNLEIWRAGK--KRSRLEN 398

QY 302 ATQSLYPLIGHAGMDWMDACSTTARRGADWTPEKDKALPKVFNLYDSVKNKDERKS 361

Db 303 EAQISIDNSKPDYREKLEAELEIRNLEIWRAGK--KRSRLEN 346

Db 298 ATQSLYPLIGHAGMDWMDACSTTARRGADWTPEKDKALPKVFNLYDSVKNKDERKS 357

Search completed: March 22, 2006, 15:27:06
Job time : 115.954 secs

QY 362 LEYNSQPDYRERYAELEIRNLEIWRAGK--RSLR 395

QY 357 ERKRSLEYNQPDYRERYAELEIRNLEIWRAGK--KRSRLEN 398

Db 358 LEFNSRKYREDIQLKELDEIDNOEIWRAGKTVGLR 393

Db 303 EAQISIDNSKPDYREKLEAELEIRNLEIWRAGK--KRSRLEN 346

RESULT 15

ABU20976 standard; protein; 347 AA.

XX ABU20976;

XX 19-JUN-2003 (first entry)

DE Protein encoded by Prokaryotic essential gene #6503.

XX Antisense; prokaryotic essential gene; cell proliferation; drug design.

XX Bacteroides fragilis.

OS WO200277183-A2.

XX 03-OCT-2002.

XX 21-MAR-2002; 2002WO-US0009107.

XX 21-MAR-2001; 2001US-00815242.

XX 06-SEP-2001; 2001US-00948993.

XX 25-OCT-2001; 2001US-0342923P.

XX 08-FEB-2002; 2002US-00072851.

XX 06-MAR-2002; 2002US-0362699P.

XX (ELIT-) ELITRA PHARM INC.

XX Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW;

XX Wall D, Trawick JD, Carr GU, Yamamoto R, Forsyth RA, Xu HH;

XX WPI; 2003-029926/02.

XX N-PSDB; ACA24846.

XX New antisense nucleic acids, useful for identifying proteins or screening

GenCore version 5.1.1.7

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OM protein - protein search, using sw model

Run on: March 22, 2006, 15:21:02 ; Search time 113.517 Seconds
(without alignments)
1528.885 Million cell updates/sec

Title: US-10-797-248a-2

Perfect score: 2071

Sequence: 1 MLTQARLLICNSRVITAKR.....RNMEIKVGKVKLRPENQ 395

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq_21.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*
- 9: Geneseqp2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2071	100.0	395	6 ABR64304	AbR64304 Acetohydr
2	2071	100.0	395	7 ADK64188	AdK64188 Disease t
3	1667	80.5	400	4 AAU15089	Aau15089 Protein e
4	1667	80.5	400	5 ABP73238	Abp73238 Candida a
5	1508.5	72.8	400	6 ABR64305	AbR64305 Acetohydr
6	1507	72.8	400	6 ABR64306	AbR64306 Acetohydr
7	1507	72.8	400	9 ADV16807	AdV16807 M grisea
8	1503	72.6	402	6 ABR64303	AbR64303 Acetohydr
9	1487.5	71.8	396	6 ABJ26477	AbJ26477 Aspergill
10	1487.5	71.8	508	6 ABJ26502	AbJ26502 Aspergill
11	1482.5	70.6	388	6 ABJ25902	AbJ25902 Aspergill
12	1462.5	70.6	500	6 ABJ25877	AbJ25877 Aspergill
13	1448.5	69.9	403	9 ADV16810	AdV16810 M grani
14	1392.5	67.2	409	7 ADB70124	AdB70124 C. neof
15	1099.5	53.1	347	6 ABU20976	AbU20976 Protein e
16	495	23.9	332	4 AAB96356	Aab96356 Putative
17	470	22.7	337	6 ABU24174	AbU24174 Protein e
18	465	22.5	331	5 ABB48168	Abb48168 Listeria
19	465	22.5	331	6 ABU32456	AbU32456 Protein e
20	461	22.3	342	4 AAU01250	Aau01250 B. subtil
21	458.5	22.1	334	4 AAG81458	Agg81458 S. epide
22	458.5	22.1	334	6 ABU42920	Abu42920 Protein e
23	458.5	22.1	339	5 ABP39068	Abp39068 Staphyloc
24	458.5	22.1	339	8 ADS07053	AdS07053 Staphyloc

ALIGNMENTS

RESULT 1

ABR64304

ID ABR64304 standard; protein; 395 AA.

XX ABR64304;

DT 16-SEP-2003 (first entry)

DE Acetohydroxyacid isomeroreductase.

XX Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase;
XX yeast.

OS Saccharomyces cerevisiae.

PN FR2829363-A1.

XX 14-MAR-2003.

PF 10-SEP-2001; 2001FR-00011689.

PR 10-SEP-2001; 2001FR-00011689.

XX (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;

DR WPI; 2003-405775/39.

PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.

XX Claim 2; Fig 1; 66pp; French.

XX The present invention relates to a method for controlling fungal disease
XX in crops by applying an inhibitor (I) of acetohydroxyacid
XX isomeroreductase. (I) are used for curative or preventative treatment of
XX a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
XX rape. The present sequence is an acetohydroxyacid isomeroreductase, used
XX to illustrate the invention

XX Sequence 395 AA;

Query Match 100.0%; Score 2071; DB 6; Length 395;

Best Local Similarity 100.0%; Pred. No. 1.3e-186;

Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSPARFVKPMITTRGLKQINFGGTVETV 60
DB 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSPARFVKPMITTRGLKQINFGGTVETV 60
QY 61 YERADWPREKLLDYFNKDTFALIGYSGQYGGQGLNLRDNLNVIIGVRKDGASWKAIAED 120
DB 61 YERADWPREKLLDYFNKDTFALIGYSGQYGGQGLNLRDNLNVIIGVRKDGASWKAIAED 120
QY 121 GWVPGKNLFTVEDAIKRGSVYNNLLSDAAQSETWPAIKPLLTGKTYLFSHGSPVPFKDL 180
DB 121 GWVPGKNLFTVEDAIKRGSVYNNLLSDAAQSETWPAIKPLLTGKTYLFSHGSPVPFKDL 180
QY 181 THVEPPKDLVDILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
DB 181 THVEPPKDLVDILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
QY 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
DB 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
QY 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
DB 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
QY 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
DB 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
RESULT 2
ADK64188
ID ADK64188 standard; protein; 395 AA.
AC ADK64188;
XX
DT 06-MAY-2004 (first entry)
XX
DE Disease treating protein complex-derived protein #1281.
XX
KW protein complex; drug target; diagnosis.
XX
OS Unidentified.
XX
PN EP1338608-A2.
XX
PD 27-AUG-2003.
XX
PF 20-DEC-2002; 2002EP-00102902.
XX
PR 20-DEC-2001; 2001EP-00130253.
XX
PA (CELL-) CELLZOME AG.
XX
PI Bauer A, Gavin A, Superti-Furga G, Kuester B, Schultz J;
PI Marzioch M, Grandi P, Krause R, Kruse U, Merino A, Bauch A;
PI Michon A, Leutwein C, Rick J;
XX
DR WPI; 2003-638460/61.
DR N-PSDB; ADK64189.
XX
PT New proteins and protein complexes from eukaryotes, useful as targets in
PT drug screening, or in diagnosing or screening for the presence of a
PT disease or disorder, or a predisposition for developing a disease or
PT disorder in a subject.
XX
PS Disclosure; SEQ ID NO 2561; 13pp; English.
XX
CC The invention relates to novel protein complexes comprising a first and a
CC second protein, or its derivative, fragment, homologue or variant. The
CC proteins are selected from given protein complexes, which are not defined
CC in the specification. The variants are encoded by nucleic acids that
CC hybridize to the nucleic acids encoding the proteins under low stringency

CC conditions. The protein complexes are useful as targets for an active
CC agent of a pharmaceutical. These protein complexes are particularly
CC useful as drug targets for the treatment or preventing of a disease or
CC disorder. The complexes and methods above are useful in diagnosing or
CC screening for the presence of a disease or disorder or a predisposition
CC for developing a disease or disorder in a subject. These are also useful
CC in screening for a drug for treatment or prevention of a disease or
CC disorder. The molecule that modulates the amount, activity or protein
CC components of the complex is useful for the manufacture of a medicament
CC for the treatment or prevention of a disease or disorder. This sequence
CC corresponds to a protein of the invention. (Note: the sequence data for
CC this patent did not form part of the printed specification but was
CC obtained from the EPO in electronic format).
XX
SQ Sequence 395 AA;
Query Match 100.0%; Score 2071; DB 7; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.3e-186;
Matches 395; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSPARFVKPMITTRGLKQINFGGTVETV 60
DB 1 MLRTQAARLICNSRVITAKRTFALATRAAAYSPARFVKPMITTRGLKQINFGGTVETV 60
QY 61 YERADWPREKLLDYFNKDTFALIGYSGQYGGQGLNLRDNLNVIIGVRKDGASWKAIAED 120
DB 61 YERADWPREKLLDYFNKDTFALIGYSGQYGGQGLNLRDNLNVIIGVRKDGASWKAIAED 120
QY 121 GWVPGKNLFTVEDAIKRGSVYNNLLSDAAQSETWPAIKPLLTGKTYLFSHGSPVPFKDL 180
DB 121 GWVPGKNLFTVEDAIKRGSVYNNLLSDAAQSETWPAIKPLLTGKTYLFSHGSPVPFKDL 180
QY 181 THVEPPKDLVDILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
DB 181 THVEPPKDLVDILVAPKSGRTVRSIFKEGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
QY 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
DB 241 GYVYQTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
QY 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
DB 301 YPLIGKYGMDYWDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNS 360
QY 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
DB 361 QPDYREKLEKELDTIRNMEIWKVKEVRKLRPENQ 395
RESULT 3
AAU15089
ID AAU15089 standard; protein; 400 AA.
XX
AC AAU15089;
XX
DT 04-DEC-2001 (first entry)
XX
DE Protein encoded by C. albicans essential gene CAYLR355C (ILVS).
XX
KW Gene identification; essential gene; GRACE; pathogenic fungus;
KW gene replacement and conditional expression; fungal infection.
XX
OS Candida albicans.
XX
PN WO200160975-A2.
XX
PD 23-AUG-2001.
XX
PF 20-FEB-2001; 2001WO-US005551.
XX
PR 18-FEB-2000; 2000US-0183534P.
XX
PA (ELIT-) ELITRA PHARM INC.

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XX Roemer T, Jiang B, Boone C, Bussey H;
XX WPI; 2001-489080/53.
XX N-PSDB; AAS23417.
XX Identifying genes essential to fungal metabolisms and identifying
XX potential therapeutic agents that target these genes.
XX Claim 43; Page 222-223; 324pp; English.
XX The present invention relates to novel methods for constructing fungal
XX strains useful for identification and validation of gene products as
XX targets for therapeutic agents, for creating a collection of identified
XX essential genes, and screening assays for the discovery of new drugs. The
XX invention provides the GRACE (gene replacement and conditional
XX expression) method for the construction of mutant organisms referred to
XX as GRACE strains of the organism. The invention can be applied to any
XX organism, particularly a pathogenic fungus e.g. Candida albicans,
XX Aspergillus fumigatus and Cryptococcus neoformans. The methods are useful
XX to identify agents that may be used in the treatment of fungal
XX infections. AAU15053-AAU15113 represent proteins encoded by C. albicans
XX essential genes
XX Sequence 400 AA;

Query Match      80.5%; Score 1667; DB 4; Length 400;
Best Local Similarity 79.1%; Pred. No. 2.2e-148;
Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;

QY 3 RTQARL--ICNSRVITAKTFAL---ATRAAAYSPPAARFVKPMITTRGLKQINFGTV 57
DB 4 RTTSMRWARLATAKATLSKRTFSLANATTRYTAASSAAKAMTPTSIRGVKTINGGTE 63
QY 58 ETYVERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRKDGASWKA 117
DB 64 EVVHERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRK-GSSWEA 122
QY 118 IEDGWVPGKDLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLYFSGHSPVF 177
DB 123 VEDGWVPGENLFEVDEAISRGTIIMDLLSDAAQSETWFWHIKPOLTEGKTLYFSGHSPVF 182
QY 178 KOLTHVEPPKDLVDVILVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVA 237
DB 183 KOLTHVEPPSNIDVILAAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAIAIA 242
QY 238 IGSYVYVOTTFERWNSDLXGERCLMGGIHGMFLAQYDVLRENGHSPSAFNETVEEAT 297
DB 243 IGSYVYVYTFERWNSDLXGERCLMGGIHGMFLAQYEVIRENGHTPPSEAFNETVEEAT 302
QY 298 QSLYPLIGKYGMDYMDACSTTARRGALDWYPIPKNAKLPVFDLYESTKNGTETKRSLE 357
DB 303 QSLYPLIGKYGMDYMDACSTTARRGALDWYPRFKDALKVPFEELYESVNGSETKRSLE 362
QY 358 FNSQPDYREKLEKELDTIRNWEIKWQKVRKLRPNQ 395
DB 363 FNSRSDYKERLEEELQIRNWEIKWQKVRKLRPNQ 400

RESULT 4
ABP73238
XX ID ABP73238 standard; protein; 400 AA.
XX AC ABP73238;
XX DT 30-JAN-2003 (first entry)
XX DE Candida albicans essential protein SEQ ID NO 7075.
XX KW Fungus; yeast; tetracycline; promoter; GRACE strain; biosynthesis;
XX KW signal transduction; DNA replication; cell division; growth;
XX KW proliferation; Candida albicans; fungicide; antifungal.

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OS Candida albicans.
XX WO200253728-A2.
XX 11-JUL-2002.
XX 26-DEC-2001; 2001WO-US049486.
XX 29-DEC-2000; 2000US-0259128P.
XX 20-FEB-2001; 2001US-00792024.
XX 22-AUG-2001; 2001US-0314050P.
XX (ELIT-) ELITRA PHARM INC.
XX Roemer T, Jiang B, Boone C, Bussey H, Ohlsen KL;
XX WPI; 2002-566694/60.
XX N-PSDB; ABZ31788.
XX Constructing strains for identifying gene products as effective targets
XX for therapeutic intervention, by inactivating in the strain one allele of
XX a gene and placing other allele of the gene under conditional expression.
XX Claim 44; SEQ ID NO 7075; 167pp + Sequence Listing; English.
XX The invention relates to constructing (M1) a strain of diploid fungal
XX cells in which both alleles of a gene are modified, comprising modifying
XX one allele by insertion or replacement by a cassette having an
XX expressible selectable marker and modifying other allele by
XX recombination, of a promoter replacement fragment with a heterologous
XX promoter, so that expression of the second allele is regulated by the
XX promoter. (M1) is useful for constructing a strain of diploid fungal
XX cells in which both alleles of a gene are modified. The diploid fungal
XX cells having both alleles modified are useful for identifying a gene that
XX is essential to the survival or growth of a fungus, a gene that
XX contributes to the virulence and/or pathogenicity of a fungus, a gene
XX that contributes to the resistance of a diploid fungus to an antifungal
XX agent, an antifungal agent that inhibits the growth of a diploid fungus
XX and for identifying a therapeutic agent for treatment of a mammalian
XX disease. (M1) is useful for identifying a compound which modulates the
XX activity of a gene product, preferably enzymatic activity, carbon
XX compound catabolism, biosynthetic, transporter, transcriptional,
XX translational, signal transduction, DNA replication and cell division
XX activity. The method is useful for identifying a compound having the
XX ability to inhibit growth or proliferation of C. albicans cells and for
XX treating infection by C. albicans. The present sequence is that of an
XX essential Candida albicans protein used in the method of the invention.
XX Note: The sequence data for this patent is not represented in the printed
XX specification but is based on sequence information supplied to Derwent by
XX the European Patent Office
XX Sequence 400 AA;

Query Match      80.5%; Score 1667; DB 5; Length 400;
Best Local Similarity 79.1%; Pred. No. 2.2e-148;
Matches 315; Conservative 42; Mismatches 35; Indels 6; Gaps 3;

QY 3 RTQARL--ICNSRVITAKTFAL---ATRAAAYSPPAARFVKPMITTRGLKQINFGTV 57
DB 4 RTTSMRWARLATAKATLSKRTFSLANATTRYTAASSAAKAMTPTSIRGVKTINGGTE 63
QY 58 ETYVERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRKDGASWKA 117
DB 64 EVVHERADWPKEKLDYFKNDTFALIGYSGYGGQLNRDNLNGLNVIIGVRK-GSSWEA 122
QY 118 IEDGWVPGKDLFTVEDAIKRGSYVMNLLSDAAQSETWPAIKPLLTGKTLYFSGHSPVF 177
DB 123 VEDGWVPGENLFEVDEAISRGTIIMDLLSDAAQSETWFWHIKPOLTEGKTLYFSGHSPVF 182
QY 178 KOLTHVEPPKDLVDVILVAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAQALAVA 237
DB 183 KOLTHVEPPSNIDVILAAPKSGRTVRSFLFKEGRGINSYAVWVNDVTGKAHEKAIAIA 242

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QY 238 IGSYVYVQTTFFREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEAT 297
DB 243 IGSYVYVQTTFFREVNSDLYGERGCLMGHGMFLAQYDVLRENGHTPSEAFNETVEAT 302
QY 298 QSLYPLIGKYGMDYDACSTTARRGALDWYPIFKNALKPVDLRENGHSPSEAFNETVE 357
DB 303 QSLYPLIGKYGMDYDACSTTARRGALDWYPIFKNALKPVDLRENGHSPSEAFNETVE 362
QY 358 FNSQPDYREKLEKELDTIRNMEIWKVGEVKRLRPENQ 395
DB 363 FNSRSDYKERLEELQTIIRNMEIWRVGEVKRLRPENQ 400

RESULT 5
ABR64305
ID ABR64305 standard; protein; 400 AA.
XX
AC ABR64305;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductase.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Neurospora crassa.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX
PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
PS Claim 2; Fig 1; 66pp; French.
XX
CC The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase. (I) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 400 AA;
Query Match 72.8%; Score 1508.5; DB 6; Length 400;
Best Local Similarity 73.6%; Pred. No. 2.1e-133;
Matches 295; Conservative 39; Mismatches 50; Indels 17; Gaps 5;
QY 4 TOAARLICNSRVITA--KRTF---ALATRAA----AYSRPAARFVKPMITTRGLKQINFG 54
DB 7 TKALRPLARGLATPAVQRRRTFVAASAVRASVAVAAPARQV-----RGVKTMDFA 60
QY 55 GIVETVYRADWPKEKLLDYFKNDTFTALIGYSGQGGQGLNLRDNGNLNVIIGVRKDGASW 114
DB 61 GHKEEVEERADWPKEKLLDYFKNDTFTALIGYSGQGGQGLNLRDNGNLNVIIGVRKDGASW 120
QY 115 KAAIEDGWPGKPLFTVEDAIKRGSVYVNNLLSDAAQSETWPAIKPLLTGKLTLYFSHGFS 174
DB 121 EDRIQGWPGKPLFDVDEAISRTIVMNLSDAAQSETWPHIKPQITGKLTLYFSHGFS 180
QY 175 PVFKDLTHVEPPKDLVILVAPKSGRTVRSFLPKRGGINSSYAVWVNDVTGKAHEKAQAL 234
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DB 181 PVFKDLTKVEVPTDVDVILVAPKSGRTVRSFLREGGINSSFAVYQDVTGRAKEKAVAL 240
QY 235 AVAIGSYVYQTTFFREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVE 294
DB 241 GVAVSGYLYETTFEKEVYSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVE 300
QY 295 EATQSLYPLIGKYGMDYDACSTTARRGALDWYPIFKNALKPVDLRENGHSPSEAFNETVE 354
DB 301 EATQSLYPLIGKYGMDYDACSTTARRGALDWYPIFKNALKPVDLRENGHSPSEAFNETVE 360
QY 355 SLEFNSQPDYREKLEKELDTIRNMEIWKVGEVKRLRPENQ 395
DB 361 SLEYNQPDYREKLEKELDTIRNMEIWRVGEVKRLRPENQ 399

RESULT 6
ABR64306
ID ABR64306 standard; protein; 400 AA.
XX
AC ABR64306;
XX
DT 16-SEP-2003 (first entry)
XX
DE Acetohydroxyacid isomeroreductase #2.
XX
KW Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.
XX
OS Magnaporthe grisea.
XX
PN FR2829363-A1.
XX
PD 14-MAR-2003.
XX
PF 10-SEP-2001; 2001FR-00011689.
XX
PR 10-SEP-2001; 2001FR-00011689.
XX
PA (AVET ) AVENTIS CROPS SCIENCE SA.
XX
PI Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;
XX WPI; 2003-405775/39.
XX
DR N-PSDB; ACC80185, ACC80186.
XX
PT Treatment of crops, useful for controlling fungi on, e.g. cereals,
PT potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
PT isomeroreductase.
XX
PS Disclosure; Page 57-58; 66pp; French.
XX
CC The present invention relates to a method for controlling fungal disease
CC in crops by applying an inhibitor (I) of acetohydroxyacid
CC isomeroreductase. (I) are used for curative or preventative treatment of
CC a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or
CC rape. The present sequence is an acetohydroxyacid isomeroreductase, used
CC to illustrate the invention
XX
SQ Sequence 400 AA;
Query Match 72.8%; Score 1507; DB 6; Length 400;
Best Local Similarity 73.2%; Pred. No. 2.9e-133;
Matches 289; Conservative 44; Mismatches 56; Indels 6; Gaps 3;
QY 2 LHTQARLICNSRVITAKRTFATATRAAAYSRAARFVKP-MITTRGLKQINFGTVEIV 60
DB 10 LRPMAQL---ATPAVQRRRTFVAASVMVRAATRAA--VAPTOQQIRGVKTMDFAGHKEQV 64
QY 61 YERADWPKEKLLDYFKNDTFTALIGYSGQGGQGLNLRDNGNLNVIIGVRKDGASWKAALIED 120
DB 65 WERADWPKEKLLDYFKNDTFTALIGYSGQGGQGLNLRDNGNLNVIIGVRKDGASWKAALIED 124
QY 121 GWVPGKPLFTVEDAIKRGSVYVNNLLSDAAQSETWPAIKPLLTGKLTLYFSHGFSVPFKDL 180
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125 GWVEKMLFEVDEISRGTVIMNLSDAQSETPALKPQITKGTLYFSGHSPVPKDL 184
 181 THVEPPKDLVDILVAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
 185 TKVEVPTDVIDILCAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 244
 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
 245 GYLYKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304
 301 YPLIGKGYMDYWDACSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFNS 360
 305 YPLIGANGMDWYECSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFNS 364
 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395
 365 QPDYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQ 399

RESULT 7

ADV16807
 ID ADV16807 standard; protein; 400 AA.

XX AC ADV16807;
 XX DT 24-FEB-2005 (first entry)
 XX DE

XX M grisea ketol-acid reductoisomerase ILV5 seqid 6.
 XX substrate inhibition; antibiotic; gene disruption;
 XX ketol-acid reductoisomerase; ILV5; enzyme.

XX Magnaporthe grisea.
 XX OS
 XX WO2004104176-A2.
 XX PD 02-DEC-2004.

XX 17-MAY-2004; 2004WO-US015404.
 XX 15-MAY-2003; 2003US-0470947P.
 XX 19-MAY-2003; 2003US-0471615P.
 XX 21-MAY-2003; 2003US-0472422P.
 XX (PARA-) PARADIGM GENETICS INC.

XX Tanzer MM, Hamer L, Adachi K, Dezwaan TM, Lo SC;
 XX Montenegro-Chamorro MV, Darveau BA, Frank SA, Heiniger RW;
 XX Mahanty SK, Pan H, Covington AS, Tarpey R, Shuster JR;
 XX WPI; 2005-021202/02.
 XX N-PSDB; ADV16805, ADV16806.

XX Identifying a test compound as a candidate for an antibiotic comprises
 XX contacting ornithine carbamoyltransferase (OCTase) or ketol-acid
 XX reductoisomerase polypeptide, or fungal pathogenicity-conferring gene
 XX with a test compound.

XX Claim 48; SEQ ID NO 6; 179pp; English.

XX The invention describes a method of identifying a test compound as a
 XX candidate for an antibiotic comprising contacting ornithine
 XX carbamoyltransferase (OCTase) or ketol-acid reductoisomerase polypeptide,
 XX or fungal pathogenicity-conferring gene with a test compound. The method
 XX comprises: contacting OCTase polypeptide, ketol-acid reductoisomerase
 XX polypeptide, or fungal pathogenicity-conferring gene with a test compound
 XX ; and detecting the presence or absence of binding between the test
 XX compound and the polypeptide or gene, where binding indicates that the
 XX test compound is a candidate for an antibiotic. Also described are: an
 XX isolated nucleic acid comprising a nucleotide sequence encoding a
 XX polypeptide having at least 50% sequence identity to, or having at least
 XX 10% of the activity of, 400, 403 or 469 amino acids; and an isolated

CC polypeptide consisting essentially of the amino acid sequence of 400, 403
 CC or 469 amino acids. The methods are useful for identifying inhibitors of
 CC ornithine carbamoyltransferase, ketol-acid reductoisomerase, and fungal
 CC pathogenicity-conferring gene as antibiotics. This is the amino acid
 CC sequence of Magnaporthe grisea ketol-acid reductoisomerase ILV5.
 XX
 XX Sequence 400 AA;

Query Match 72.8%; Score 1507; DB 9; Length 400;
 Best Local Similarity 73.2%; Pred. No. 2.9e-133;
 Matches 289; Conservative 44; Mismatches 56; Indels 6; Gaps 3;

QY 2 LRTOAARLICNSRVITAKTTFALATRAAYSRPAARFVKP-MITTRGLKQINEGGVETV 60
 DB 10 LRPMARQL---ATPAVQRRTFVAASSMVRATRKAA--VAPTQQOIRGVKTMDFAGHKEQV 64
 QY 61 YERADWPKEKLDYFKNDTFALIGYSGQYGGQGLNRDNLNGLNVIIGVRKDGASWKAIAIED 120
 DB 65 WERADWPKEKLDYFKNDTFALIGYSGQYGGQGLNRDNLNGLNVIIGVRKDGASWKAIAIED 124
 QY 121 GWVPGKNLFTVEDAIKRGSYVMNLLSDAAQSETPALKPQITKGTLYFSGHSPVPKDL 180
 DB 125 GWVPGKNLFEVDEAISRGTVIMNLSDAQSETPALKPQITKGTLYFSGHSPVPKDL 184
 QY 181 THVEPPKDLVDILVAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 240
 DB 185 TKVEVPTDVIDILCAPKSGRTVRSFKGGRGINSYAVVNDVTGKAHEKAQALAVAIGS 244
 QY 241 GYVYQTTFFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300
 DB 245 GYLYKTTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304
 QY 301 YPLIGKGYMDYWDACSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFNS 360
 DB 305 YPLIGANGMDWYECSTTARRGALDWYPIFKNALKPVFDLYSTKNGTETKRSLEFNS 364
 QY 361 QPDYREKLEKELDTIRNMEIWKVGEVRLRPENQ 395
 DB 365 QPDYREKYEAEEMIEIRNLEIWRAGKAVRSLRPENQ 399

RESULT 8

ABR64303
 ID ABR64303 standard; protein; 402 AA.

XX AC ABR64303;

XX DT 16-SEP-2003 (first entry)

XX DE Acetohydroxyacid isomeroreductase #1.

XX Enzyme; antifungal; fungal disease; acetohydroxyacid isomeroreductase.

XX Magnaporthe grisea.

XX FN FR2829363-A1.

XX PD 14-MAR-2003.

XX PF 10-SEP-2001; 2001FR-00011689.

XX PR 10-SEP-2001; 2001FR-00011689.

XX (AVET) AVENTIS CROPS SCIENCE SA.

XX Dumas R, Lebrun MH, Zundel JL, Effantin G, Morin V;

XX WPI; 2003-405775/39.

XX Treatment of crops, useful for controlling fungi on, e.g. cereals,
 XX potato, cotton or rape, comprises applying inhibitor of acetohydroxy acid
 XX isomeroreductase.

PS	Claim 2; Fig 1; 66pp; French.	
XX	The present invention relates to a method for controlling fungal disease	
CC	in crops by applying an inhibitor (I) of acetohydroxyacid	
CC	isomeroreductase. (I) are used for curative or preventative treatment of	
CC	a wide range of fungal diseases on crops, e.g. cereals, potato, cotton or	
CC	rape. The present sequence is an acetohydroxyacid isomeroreductase, used	
CC	to illustrate the invention	
XX		
SQ	Sequence 402 AA;	
	Query Match 72.6%; Score 1503; DB 6; Length 402;	
	Best Local Similarity 72.9%; Pred. No. 7.1e-133;	
	Matches 288; Conservative 45; Mismatches 56; Indels 6; Gaps 3;	
Qy	2 LRTQAARLNCNSRVITAKRTFALATRAAAYSRPAAREVKP-MITTRGLKQINFGTVEY 60	
Db	10 LRPWARGL---ATPAVQRSSFVAASSMVRATRXAA--VAPTQQIRGVKTMDFAGHKEQV 64	
Qy	61 YERADWPREKLLDYFKNDTFALIGYSGYGGQGLNRDNLNVIIGVRKDGASWKAIED 120	
Db	65 WERADWPREKLLDYFKNDTFALIGYSGYGGQGLNRDNLNVIIGVRKDGASWKAIED 124	
Qy	121 GWPGKGLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHSPVPKDL 180	
Db	125 GWPGKGLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHSPVPKDL 184	
Qy	181 THVEPPKDLVDILVAPKSGRTVRSIFKEGRGINSSYAVVNDVTGKAHEKAQALAVAIGS 240	
Db	185 TKVEVPTDVIDLCAKSGRTVRSIFKEGRGINSSYAVVNDVTGKAHEKAQALAVAIGS 244	
Qy	241 GYVYQTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSL 300	
Db	245 GYLYKTTFEKEVYSDLYGERGCLMGHGMFLAQYEVLRERGHSPSEAFNETVEEATQSL 304	
Qy	301 YPLIGKYGMDYDACSTTARRGALDWPYIPFKNALKPVFODLYESTKNGTETKRSLEFNS 360	
Db	305 YPLIGANGMDYDACSTTARRGALDWPYIPFKNALKPVFODLYESTKNGTETKRSLEFNS 364	
Qy	361 QPDYREKLEKELDIRNMEIWKVGEVKRLRPENQ 395	
Db	365 QPDYREKYEAMEIRNLEIWRAGKAVRSILRPENQ 399	
RESULT 9		
ABJ26477	standard; protein; 396 AA.	
ID	ABJ26477	
AC	ABJ26477;	
XX	16-APR-2003 (first entry)	
DT	Aspergillus fumigatus essential gene protein #1135.	
DE	Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;	
XX	cancer; contamination; biofilm; antibody; immune response.	
KW	Aspergillus fumigatus.	
OS	WO200286090-A2.	
PN	31-OCT-2002.	
XX	23-APR-2002; 2002WO-US013142.	
PF	23-APR-2001; 2001US-0285697P.	
PR	27-APR-2001; 2001US-0287066P.	
PR	05-JUN-2001; 2001US-0295890P.	
PR	09-JUL-2001; 2001US-0303899P.	
PR	31-AUG-2001; 2001US-0316362P.	
XX	(ELIT-) ELITRA PHARM INC.	
PA		
XX		

PI	Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;	
XX	WPI; 2003-093124/08.	
DR	New purified or isolated nucleic acids of essential genes of Aspergillus	
XX	fumigatus, useful for treating or preventing infections by A. fumigatus,	
PT	or for treating a non-infectious disease in a subject e.g. cancer.	
XX	Disclosure; Page: 175pp; English.	
PS	The invention relates to novel purified or isolated nucleic acids of	
XX	essential genes of Aspergillus fumigatus. The isolated nucleic acids of	
CC	the invention are used to treat or prevent infections by a pathogenic	
CC	organism such as A. fumigatus, to treat a non-infectious disease in a	
CC	subject (e.g. cancer), to prevent or contain contamination of an object	
CC	by A. fumigatus, or to prevent or inhibit formation on a surface of a	
CC	biofilm comprising A. fumigatus. The polynucleotides are useful for	
CC	expressing recombinant protein for characterisation, screening or	
CC	therapeutic use, as markers for host tissues in which the pathogenic	
CC	organisms invade or reside, for comparing with the DNA sequence of A.	
CC	fumigatus to identify duplicated genes or paralogues having the same or	
CC	similar biochemical activity and/or function, for comparing with DNA	
CC	sequences of other related or distant pathogenic organisms to identify	
CC	potential orthologous essential or virulence genes, for selecting and	
CC	making oligomers for attachment to a nucleic acid array for examination	
CC	of expression patterns, for raising anti-protein antibodies, as an	
CC	antigen to raise anti-DNA antibodies or to elicit another immune	
CC	response, and for identifying polynucleotides encoding the other protein	
CC	with which binding occurs or to identify inhibitors of the binding	
CC	interaction. The polypeptides may be used to raise antibodies or to	
CC	elicit immune response, as a reagent in assays designed to quantitatively	
CC	determine levels of the protein in biological fluids, as a marker for	
CC	host tissues in which pathogenic organism invade or reside, and to	
CC	isolate correlative receptors or ligands in the case of virulence	
CC	factors. This sequence represents a protein of one of the essential genes	
CC	of Aspergillus fumigatus of the invention	
XX		
SQ	Sequence 396 AA;	
	Query Match 71.8%; Score 1487.5; DB 6; Length 396;	
	Best Local Similarity 71.6%; Pred. No. 2e-131;	
	Matches 280; Conservative 46; Mismatches 62; Indels 3; Gaps 1;	
Qy	5 QAARLNCNSRVITAKRTFALATRAAAYSRPAARVFKPMITTRGLKQINFGTVEYVERA 64	
Db	8 RALRL---ARVAAPRTVISAAALPRALAKAATRVAASTAPVRGVKTIAPADSKETVYERA 64	
Qy	65 DWPREKLLDYFKNDTFALIGYSGYGGQGLNRDNLNVIIGVRKDGASWKAIEDGWTP 124	
Db	65 DWPREKLLDYFKNDTFALIGYSGYGGQGLNRDNLNVIIGVRKDGASWKAIEDGWTP 124	
Qy	125 GKNLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHSPVPKDLTHVE 184	
Db	125 GKNLFTVEDAIKRGSVVMNLLSDAAQSETWPAIKPLLTKGKTLFSGHSPVPKDLTHVE 184	
Qy	185 PKDLVDILVAPKSGRTVRSIFKEGRGINSSYAVVNDVTGKAHEKAQALAVAIGSGYVY 244	
Db	185 VPKDVIDILVAPKSGRTVRSIFKEGRGINSSYAVVNDVTGKAHEKAQALAVAIGSGYVY 244	
Qy	245 QTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI 304	
Db	245 ETTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEEATQSLYPLI 304	
Qy	305 GKYGMDYDACSTTARRGALDWPYIPFKNALKPVFODLYESTKNGTETKRSLEFNSQPDY 364	
Db	305 GANGMDYDACSTTARRGALDWPYIPFKNALKPVFODLYESTKNGTETKRSLEFNSQPDY 364	
Qy	365 REKLEKELDIRNMEIWKVGEVKRLRPENQ 395	
Db	365 REKYEKEMQDIRLEIWRAGKAVGSLRPENQ 395	
RESULT 10		

ABJ26502	DB	120	RALRL---ARVAAPRTVISALPRPALAKAATRAAATASTAPVRGVKTIATFADSKETVTERA	176
ID ABJ26502 standard; protein; 508 AA.				
XX				
AC ABJ26502;	QY	65	DWPREKLLDYFNKNDTTFALIGYSGQYGGQGLNLRDNGLNVIIGVRKDGASWKAATIEDGWVP	124
XX				
XX				
DT 16-APR-2003 (first entry)	DB	177	DWPREKLOEYFNKNDTTFALIGYSGQYGGQGLNLRDNGLNVIIGVRKDGASWKAATIEDGWVP	236
XX				
XX				
DE Aspergillus fumigatus essential gene protein #1160.	QY	125	GKNLFTVEDAIKRGSVYNNLLSDAAQSETWPAIKPLITKTKTLYFSHGFSFVKDLTHVE	184
XX				
XX				
KW Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;	DB	237	GKNLFDLTEAVQVGTIVNNLLSDAAQSETWPAIKPLITKTKTLYFSHGFSFVKDLTHVE	296
KW cancer; contamination; biofilm; antibody; immune response.				
XX				
OS Aspergillus fumigatus.	QY	185	PKXDLVILVAPKSGRTVRSKPKGGRGINSVAVVNDVTGKAHKAQAALAVAGSGVY	244
XX				
XX				
PN WO200286090-A2.	DB	297	VPKXDLVILVAPKSGRTVRSKPKGGRGINSVAVVNDVTGKAHKAQAALAVAGSGVY	356
XX				
XX				
PD 31-OCT-2002.	QY	245	QTTFEREVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEATQSLYPLI	304
XX				
XX				
PF 23-APR-2002; 2002WO-US013142.	DB	357	ETTKEVNSDLYGERGCLMGHGMFLAQYDVLRENGHSPSEAFNETVEATQSLYPLI	416
XX				
XX				
PR 23-APR-2001; 2001US-0285697P.	QY	305	GKYGMDYMDACSTTARRGALDWYPIFKALKKPVFDLYESTKNGTETTKSLEFNSQPDY	364
PR 27-APR-2001; 2001US-0287066P.				
PR 05-JUN-2001; 2001US-0295890P.	DB	417	GANGMDMYAACSTTARRGALDWYPIFKALKKPVFDLYESTKNGTETTKSLEFNSQPDY	476
PR 09-JUL-2001; 2001US-0303899P.				
PR 31-AUG-2001; 2001US-0316362P.	QY	365	REKLEKELDTIRNMEIKVKEVRKLRPENQ	395
XX				
PA (ELIT-) ELITRA PHARM INC.	DB	477	REKLEKELDTIRNMEIKVKEVRKLRPENQ	507
XX				
PI Jiang B, Tishkoff D, Zamudio C, Eroshkin AM, Hu W, Lemieux SM;				
XX				
XX				
DR WPI; 2003-093124/08.				
XX				
XX				
PT New purified or isolated nucleic acids of essential genes of Aspergillus				
PT fumigatus, useful for treating or preventing infections by A. fumigatus,				
XX				
XX				
PS Disclosure; Page; 175pp; English.				
XX				
CC The invention relates to novel purified or isolated nucleic acids of				
CC essential genes of Aspergillus fumigatus. The isolated nucleic acids of				
CC the invention are used to treat or prevent infections by a pathogenic				
CC organism such as A. fumigatus, to treat a non-infectious disease in a				
CC subject (e.g. cancer), to prevent or contain contamination of an object				
CC by A. fumigatus, or to prevent or inhibit formation on a surface of a				
CC biofilm comprising A. fumigatus. The polynucleotides are useful for				
CC expressing recombinant protein for characterisation, screening or				
CC therapeutic use, as markers for host tissues in which the pathogenic				
CC organisms invade or reside, for comparing with the DNA sequence of A.				
CC fumigatus to identify duplicated genes or paralogues having the same or				
CC similar biochemical activity and/or function, for comparing with the DNA				
CC sequences of other related or distant pathogenic organisms to identify				
CC potential orthologous essential or virulence genes, for selecting and				
CC making oligomers for attachment to a nucleic acid array for examination				
CC of expression patterns, for raising anti-protein antibodies, as an				
CC antigen to raise anti-DNA antibodies or to elicit another immune				
CC response, and for identifying polynucleotides encoding the other protein				
CC with which binding occurs or to identify inhibitors of the binding				
CC interaction. The polypeptides may be used to raise antibodies or to				
CC elicit immune response, as a reagent in assays designed to quantitatively				
CC determine levels of the protein in biological fluids, as a marker for				
CC host tissues in which pathogenic organism invade or reside, and to				
CC isolate correlative receptors or ligands in the case of virulence				
CC factors. This sequence represents a protein of one of the essential genes				
CC of Aspergillus fumigatus of the invention				
XX				
SQ Sequence 508 AA;				
Query Match				
Best Local Similarity				
Matches 280; Conservative 46; Mismatches 62; Indels 3; Gaps 1;				
QY 5 QAARLCSNRSVITAKRTFALATRAAAYSRPAARFVKPMITTRGLKQINFGTIVTERA 64				

expressing recombinant protein for characterisation, screening or therapeutic use, as markers for host tissues in which the pathogenic organisms invade or reside, for comparing with the DNA sequence of A. fumigatus to identify duplicated genes or paralogues having the same or similar biochemical activity and/or function, for comparing with DNA sequences of other related or distant pathogenic organisms to identify potential orthologous essential or virulence genes, for selecting and making oligomers for attachment to a nucleic acid array for examination of expression patterns, for raising anti-protein antibodies, as an antigen to raise anti-DNA antibodies or to elicit another immune response, and for identifying polynucleotides encoding the other protein with which binding occurs or to identify inhibitors of the binding interaction. The polypeptides may be used to raise antibodies or to elicit immune response, as a reagent in assays designed to quantitatively determine levels of the protein in biological fluids, as a marker for host tissues in which pathogenic organism invade or reside, and to isolate correlative receptors or ligands in the case of virulence factors. This sequence represents a protein of one of the essential genes of Aspergillus fumigatus of the invention

Sequence 388 AA:

Query Match	70.6%;	Score 1462.5;	DB 6;	Length 388;
Best Local Similarity	71.6%;	Pred. No. 4.5e-129;		
Matches 275;	Conservative 46;	Mismatches 60;	Indels 3;	Gaps 1;
Qy	5	QAARLCNSRVITAKRTIFALATRAAAAYSRPAARFKVPMITTRGLKQINFGCTVETVVERA	64	
Db	8	RAURL-----ARVAAPRTVISALPPALAKAATRAVAASTAPVRGVKTIATAFDSKETVVERA	64	
Qy	65	DWPREKLLDYFNKDTFALIGYSGQYGGQLNRDLNGLNVIIGVRKDGASWKAALIEDGWVP	124	
Db	65	DWPREKLOEYFNKDTLALIGYSGQHGQGLNRDQGLNVIIGVRKDGASWKEAIQDGWIP	124	
Qy	125	GKNLFTVEDAIKRGSYWNLLISDAAQSETWPAIKPLLTKGKTLVFSHGCFSPVFKDLTHVE	184	
Db	125	GKNLFDTEAVQKGTIWNLLISDAAQSETWPTLKPLITKGKTLVFSHGFSVPFVKELTKVD	184	
Qy	185	PPKDLDVILVAPKSGRTRVSLPKEGRGINSYAVMNDVTCKAHEKAQALAVAGSGVYV	244	
Db	185	VPKDQDVILVAPKSGRTRVTLFREGRGINSIIAVYQDVTCKAKEKAIAMGVAVSGVLY	244	
Qy	245	QTTFERVNSDLYGERCLMGHIGMFLAQYDVLRENGHSSEAFNETVEATQSLYPLI	304	
Db	245	ETTPEKEVYSDLYGERCLMGHIGMFLAQYEVLRERGHSPSEAFNETVEEATQSLYPLI	304	
Qy	305	GKYGMDYMYDACSTTARRGALDWYPIFKNALKPVFDLYESTKNGTETKRSLEFNSPQDY	364	
Db	305	GANGMDWMYAACSTTARRGALDWSRPFDTLKPINELYDSVRGTETKRSLEYNQKDY	364	
Qy	365	REKLEKELDTIRNMEIWKVQKEVR	388	
Db	365	REKYEKEMQDIRDLDEIWRAGKAVR	388	

RESULT 12	
ABJ25877	
ID	ABJ25877 standard; protein; 500 AA.
XX	
XX	ABJ25877;
XX	
XX	AC
XX	
XX	16-APR-2003 (first entry)
XX	
XX	Aspergillus fumigatus essential gene protein #535.
DE	
XX	
XX	
KW	Fungicide; cytostatic; essential gene; Aspergillus fumigatus; infection;
KW	cancer; contamination; biofilm; antibody; immune response.
XX	
XX	Aspergillus fumigatus.
OS	
XX	
XX	WO200286090-A2.
PN	
XX	
XX	
PD	31-OCT-2002.

[illegible]

Query Match	69.9%;	Score 1448.5;	DB 9;	Length 403;
Best Local Similarity	72.0%;	Pred. No. 1e-127;		

